



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Atty. Docket No: 15966-776CIP

The patent application of

GERLACH, VALERIE L. et al.

Serial No. 09/898,570

Filed: July 3, 2001

For: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
USING THE SAME

STATEMENT TO SUPPORT FILING AND SUBMISSION IN
ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents
Washington, D.C. 20231
Box SEQUENCE

Sir:

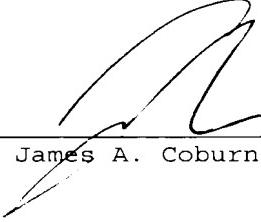
In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

1. the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not include new matter;
2. the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same; and
3. all statements made herein of their own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United

Serial No. 09/898,570

States Code and that such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

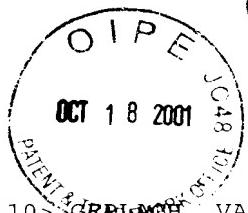
Respectfully submitted,


James A. Coburn

Oct. 1, 2001

Date

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SEQUENCE LISTING

<110> GERRIANCE, VALERIE L.
ELLERMAN, KAREN
MACDOUGALL, JOHN R.
SMITHSON, GLENNDA

<120> NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND
METHODS OF USING THE SAME

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Cys Tyr His Asp Ser Glu Ile Asp Met Asp Gln Thr Ser Leu Ser Leu
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<213> Unknown Organism

<220>
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Z97832_B.0.704

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Thr Gly Val His Cys Thr Cys Pro Val Gly Phe Met Leu Gln Pro Asp
35 40 45

Arg Lys Thr Cys Lys Asp Ile Asp Glu Cys Arg Leu Asn Asn Gly Gly
50 55 60

Cys Asp His Ile Cys Arg Asn Thr Val Gly Ser Phe Glu Cys Ser Cys
65 70 75 80

Lys Lys Gly Tyr Lys Leu Leu Ile Asn Glu Arg Asn Cys Gln Asp Ile
85 90 95

Asp Glu Cys Ser Phe Asp Arg Thr Cys Asp His Ile Cys Val Asn Thr
100 105 110

Pro Gly Ser Phe Gln Cys Leu Cys His Arg Gly Tyr Leu Leu Tyr Gly
115 120 125

Ile Thr His Cys Gly Asp Val Asp Glu Cys Ser Ile Asn Arg Gly Gly
130 135 140

Cys Arg Phe Gly Cys Ile Asn Thr Pro Gly Ser Tyr Gln Cys Thr Cys
145 150 155 160

Pro Ala Gly Gln Gly Arg Leu His Trp Asn Gly Lys Asp Cys Thr Glu
165 170 175

Pro Leu Lys Cys Gln Gly Ser Pro Gly Ala Ser Lys Ala Met Leu Ser
180 185 190

Cys Asn Arg Ser Gly Lys Lys Asp Thr Cys Ala Leu Thr Cys Pro Ser
195 200 205

Arg Ala Arg Phe Leu Pro Glu Ala Ala Val Leu Ser Ile Lys Gln Arg
210 215 220

Ala Ser Phe Lys Ile Lys Asp Ala Lys Cys Arg Leu His Leu Arg Asn
225 230 235 240

Lys Gly Lys Thr Glu Glu Ala Gly Arg Thr Thr Gly Pro Gly Gly Ala
245 250 255

Pro Cys Ser Glu Cys Gln Val Thr Phe Ile His Leu Lys Cys Asp Ser
 260 265 270
 Ser Arg Lys Gly Lys Gly Arg Arg Ala Arg Thr Pro Pro Gly Lys Glu
 275 280 285
 Val Thr Arg Leu Thr Leu Glu Leu Glu Ala Glu Val Arg Ala Glu Glu
 290 295 300
 Thr Thr Ala Ser Cys Gly Leu Pro Cys Leu Arg Gln Arg Met Glu Arg
 305 310 315 320
 Arg Leu Lys Gly Ser Leu Lys Met Leu Arg Lys Ser Ile Asn Gln Asp
 325 330 335
 Arg Phe Leu Leu Arg Leu Ala Gly Leu Asp Tyr Glu Leu Ala His Lys
 340 345 350
 Pro Gly Leu Val Ala Gly Glu Arg Ala Glu Pro Met Glu Ser Cys Arg
 355 360 365
 Pro Gly Gln His Arg Ala Gly Thr Lys Cys Val Ser Cys Pro Gln Gly
 370 375 380
 Thr Tyr Tyr His Gly Gln Thr Glu Gln Cys Val Pro Cys Pro Ala Gly
 385 390 395 400
 Thr Phe Gln Glu Arg Glu Gly Gln Leu Ser Cys Asp Leu Cys Pro Gly
 405 410 415
 Ser Asp Ala His Gly Pro Leu Gly Ala Thr Asn Val Thr Thr Cys Ala
 420 425 430
 Gly Gln Cys Pro Pro Gly Gln His Ser Val Asp Gly Phe Lys Pro Cys
 435 440 445
 Gln Pro Cys Pro Arg Gly Thr Tyr Gln Pro Glu Ala Gly Arg Thr Leu
 450 455 460
 Cys Phe Pro Cys Gly Gly Leu Thr Thr Lys His Glu Gly Ala Ile
 465 470 475 480
 Ser Phe Gln Asp Cys Asp Thr Lys Val Gln Cys Ser Pro Gly His Tyr
 485 490 495
 Tyr Asn Thr Ser Ile His Arg Cys Ile Arg Cys Ala Met Gly Ser Tyr
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 Gln Pro Asp Phe Arg Gln Asn Phe Cys Ser Arg Cys Pro Gly Asn Thr
 515 520 525
 Ser Thr Asp Phe Asp Gly Ser Thr Ser Val Ala Gln Cys Lys Asn Arg
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Asn Tyr Pro Gly Asn Tyr Pro Ala Gly Val Glu Cys Ile Trp Asn Ile
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 Asn Pro Pro Pro Lys Arg Lys Ile Leu Ile Val Val Pro Glu Ile Phe
 580 585 590
 Leu Pro Ser Glu Asp Glu Cys Gly Asp Val Leu Val Met Arg Lys Asn
 595 600 605
 Ser Ser Pro Ser Ser Ile Thr Thr Tyr Glu Thr Cys Gln Thr Tyr Glu
 610 615 620
 Arg Pro Ile Ala Phe Thr Ala Arg Ser Arg Lys Leu Trp Ile Asn Phe
 625 630 635 640
 Lys Thr Ser Glu Ala Asn Ser Ala Arg Gly Phe Gln Ile Pro Tyr Val
 645 650 655
 Thr Tyr Asp Glu Asp Tyr Glu Gln Leu Val Glu Asp Ile Val Arg Asp
 660 665 670
 Gly Arg Leu Tyr Ala Ser Glu Asn His Gln Glu Ile Leu Lys Asp Lys
 675 680 685
 Lys Leu Ile Lys Ala Phe Phe Glu Val Leu Ala His Pro Gln Asn Tyr
 690 695 700
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<220>
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 Z97832_B.0.707

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<213> Unknown Organism

<220>
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Z97832 B.O.707

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 35 40 45

 Gly Gly Ile Ala Cys Glu Cys Arg Pro Gly Phe Glu Leu Thr Lys Asn
 50 55 60

 Gln Arg Asp Cys Lys Leu Thr Cys Asn Tyr Gly Asn Gly Gly Cys Gln
 65 70 75 80

 His Thr Cys Asp Asp Thr Glu Gln Gly Pro Arg Cys Gly Cys His Ile
 85 90 95

 Lys Phe Val Leu His Thr Asp Gly Lys Thr Cys Ile Gly Glu Arg Arg
 100 105 110

 Leu Glu Gln His Ile Pro Thr Gln Ala Val Ser Asn Glu Thr Cys Ala
 115 120 125

 Val Asn Asn Gly Gly Cys Asp Ser Lys Cys His Asp Ala Ala Thr Gly
 130 135 140

 Val His Cys Thr Cys Pro Val Gly Phe Met Leu Gln Pro Asp Arg Lys
 145 150 155 160

 Thr Cys Lys Asp Ile Asp Glu Cys Arg Leu Asn Asn Gly Gly Cys Asp
 165 170 175

 His Ile Cys Arg Asn Thr Val Gly Ser Phe Glu Cys Ser Cys Lys Lys
 180 185 190

Gly Tyr Lys Leu Leu Ile Asn Glu Arg Asn Cys Gln Asp Ile Asp Glu
 195 200 205
 Cys Ser Phe Asp Arg Thr Cys Asp His Ile Cys Val Asn Thr Pro Gly
 210 215 220
 Ser Phe Gln Cys Leu Cys His Arg Gly Tyr Leu Leu Tyr Gly Ile Thr
 225 230 235 240
 His Cys Gly Asp Val Asp Glu Cys Ser Ile Asn Arg Gly Gly Cys Arg
 245 250 255
 Phe Gly Cys Ile Asn Thr Pro Gly Ser Tyr Gln Cys Thr Cys Pro Ala
 260 265 270
 Gly Gln Gly Arg Leu His Trp Asn Gly Lys Asp Cys Thr Glu Pro Leu
 275 280 285
 Lys Cys Gln Gly Ser Pro Gly Ala Ser Lys Ala Met Leu Ser Cys Asn
 290 295 300
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 305 310 315 320
 Arg Phe Leu Pro Glu Ala Ala Val Leu Ser Ile Lys Gln Arg Ala Ser
 325 330 335
 Phe Lys Ile Lys Asp Ala Lys Cys Arg Leu His Leu Arg Asn Lys Gly
 340 345 350
 Lys Thr Glu Glu Ala Gly Arg Thr Thr Gly Pro Gly Gly Ala Pro Cys
 355 360 365
 Ser Glu Cys Gln Val Thr Phe Ile His Leu Lys Cys Asp Ser Ser Arg
 370 375 380
 Lys Gly Lys Gly Arg Arg Ala Arg Thr Pro Pro Gly Lys Glu Val Thr
 385 390 395 400
 Arg Leu Thr Leu Glu Leu Glu Ala Glu Val Arg Ala Glu Glu Thr Thr
 405 410 415
 Ala Ser Cys Gly Leu Pro Cys Leu Arg Gln Arg Met Glu Arg Arg Leu
 420 425 430
 Lys Gly Ser Leu Lys Met Leu Arg Lys Ser Ile Asn Gln Asp Arg Phe
 435 440 445
 Leu Leu Arg Leu Ala Gly Leu Asp Tyr Glu Leu Ala His Lys Pro Gly
 450 455 460
 Leu Val Ala Gly Glu Arg Ala Glu Pro Met Glu Ser Cys Arg Pro Gly
 465 470 475 480
 Gln His Arg Ala Gly Thr Lys Cys Val Ser Cys Pro Gln Gly Thr Tyr
 485 490 495

Tyr His Gly Gln Thr Glu Gln Cys Val Pro Cys Pro Ala Gly Thr Phe
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 Gln Glu Arg Glu Gly Gln Leu Ser Cys Asp Leu Cys Pro Gly Ser Asp
 515 520 525
 Ala His Gly Pro Leu Gly Ala Thr Asn Val Thr Thr Cys Ala Gly Gln
 530 535 540
 Cys Pro Pro Gly Gln His Ser Val Asp Gly Phe Lys Pro Cys Gln Pro
 545 550 555 560
 Cys Pro Arg Gly Thr Tyr Gln Pro Glu Ala Gly Arg Thr Leu Cys Phe
 565 570 575
 Pro Cys Gly Gly Leu Thr Thr Lys His Glu Gly Ala Ile Ser Phe
 580 585 590
 Gln Asp Cys Asp Thr Lys Val Gln Cys Ser Pro Gly His Tyr Tyr Asn
 595 600 605
 Thr Ser Ile His Arg Cys Ile Arg Cys Ala Met Gly Ser Tyr Gln Pro
 610 615 620
 Asp Phe Arg Gln Asn Phe Cys Ser Arg Cys Pro Gly Asn Thr Ser Thr
 625 630 635 640
 Asp Phe Asp Gly Ser Thr Ser Val Ala Gln Cys Lys Asn Arg Gln Cys
 645 650 655
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 660 665 670
 Pro Gly Asn Tyr Pro Ala Gly Val Glu Cys Ile Trp Asn Ile Asn Pro
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 755 760 765
 Asp Glu Asp Tyr Glu Gln Leu Val Glu Asp Ile Val Arg Asp Gly Arg
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 785 790 795 800

Ile Lys Ala Phe Phe Glu Val Leu Ala His Pro Gln Asn Tyr Phe Lys
 805 810 815

Tyr Thr Glu Lys His Lys Glu Met Leu Pro Lys Ser Phe Ile Lys Leu
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Leu Arg Ser Lys Val Ser Ser Phe Leu Arg Pro Tyr Lys
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<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
 Z97832_B_1

<400> 13

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 <211> 974
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: POLYX
 Z97832_B_1

<400> 14
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His Ala Arg Ala Ala Gln Tyr Ser Lys Ala Ala Gln Asp Val Asp Glu
 20 25 30

Cys Val Glu Gly Thr Asp Asn Cys His Ile Asp Ala Ile Cys Gln Asn
 35 40 45

Thr Pro Arg Ser Tyr Lys Cys Ile Cys Lys Ser Gly Tyr Thr Gly Asp
 50 55 60

Gly Lys His Cys Lys Asp Val Asp Glu Cys Glu Arg Glu Asp Asn Ala
 65 70 75 80

Gly Cys Val His Asp Cys Val Asn Ile Pro Gly Asn Tyr Arg Cys Thr
 85 90 95

Cys Tyr Asp Gly Phe His Leu Ala His Asp Gly His Asn Cys Leu Asp
 100 105 110

Val Asp Glu Cys Ala Glu Gly Asn Gly Gly Cys Gln Gln Ser Cys Val
 115 120 125

Asn Met Met Gly Ser Tyr Glu Cys His Cys Arg Glu Gly Phe Phe Leu
 130 135 140

Ser Asp Asn Gln His Thr Cys Ile Gln Arg Pro Glu Glu Gly Met Asn
 145 150 155 160

Cys Met Asn Lys Asn His Gly Cys Ala His Ile Cys Arg Glu Thr Pro
 165 170 175

Lys Gly Gly Ile Ala Cys Glu Cys Arg Pro Gly Phe Glu Leu Thr Lys
 180 185 190

Asn Gln Arg Asp Cys Lys Leu Thr Cys Asn Tyr Gly Asn Gly Gly Cys
 195 200 205

Gln His Thr Cys Asp Asp Thr Glu Gln Gly Pro Arg Cys Gly Cys His
 210 215 220

Ile Lys Phe Val Leu His Thr Asp Gly Lys Thr Cys Ile Gly Glu Arg
 225 230 235 240

Arg Leu Glu Gln His Ile Pro Thr Gln Ala Val Ser Asn Glu Thr Cys
 245 250 255

Ala Val Asn Asn Gly Gly Cys Asp Ser Lys Cys His Asp Ala Ala Thr
 260 265 270

Gly Val His Cys Thr Cys Pro Val Gly Phe Met Leu Gln Pro Asp Arg
 275 280 285

Lys Thr Cys Lys Asp Ile Asp Glu Cys Arg Leu Asn Asn Gly Gly Cys
 290 295 300

Asp His Ile Cys Arg Asn Thr Val Gly Ser Phe Glu Cys Ser Cys Lys
 305 310 315 320

Lys Gly Tyr Lys Leu Leu Ile Asn Glu Arg Asn Cys Gln Asp Ile Asp
 325 330 335

Glu Cys Ser Phe Asp Arg Thr Cys Asp His Ile Cys Val Asn Thr Pro
 340 345 350

Gly Ser Phe Gln Cys Leu Cys His Arg Gly Tyr Leu Leu Tyr Gly Ile
 355 360 365

Thr His Cys Gly Asp Val Asp Glu Cys Ser Ile Asn Arg Gly Gly Cys
 370 375 380

Arg Phe Gly Cys Ile Asn Thr Pro Gly Ser Tyr Gln Cys Thr Cys Pro
 385 390 395 400

Ala Gly Gln Gly Arg Leu His Trp Asn Gly Lys Asp Cys Thr Glu Pro
 405 410 415

Leu Lys Cys Gln Gly Ser Pro Gly Ala Ser Lys Ala Met Leu Ser Cys
 420 425 430

Asn Arg Ser Gly Lys Lys Asp Thr Cys Ala Leu Thr Cys Pro Ser Arg
 435 440 445

Ala Arg Phe Leu Pro Glu Ala Ala Val Leu Ser Ile Lys Gln Arg Ala
 450 455 460

Ser Phe Lys Ile Lys Asp Ala Lys Cys Arg Leu His Leu Arg Asn Lys
 465 470 475 480

Gly Lys Thr Glu Glu Ala Gly Arg Thr Thr Gly Pro Gly Gly Ala Pro
 485 490 495

Cys Ser Glu Cys Gln Val Thr Phe Ile His Leu Lys Cys Asp Ser Ser
 500 505 510

Arg Lys Gly Lys Gly Arg Arg Ala Arg Thr Pro Pro Gly Lys Glu Val
 515 520 525

Thr Arg Leu Thr Leu Glu Leu Glu Ala Glu Val Arg Ala Glu Glu Thr
 530 535 540

Thr Ala Ser Cys Gly Leu Pro Cys Leu Arg Gln Arg Met Glu Arg Arg
 545 550 555 560

Leu Lys Gly Ser Leu Lys Met Leu Arg Lys Ser Ile Asn Gln Asp Arg
 565 570 575

Phe Leu Leu Arg Leu Ala Gly Leu Asp Tyr Glu Leu Ala His Lys Pro
 580 585 590

Gly Leu Val Ala Gly Glu Arg Ala Glu Pro Met Glu Ser Cys Arg Pro
 595 600 605

Gly Gln His Arg Ala Gly Thr Lys Cys Val Ser Cys Pro Gln Gly Thr
 610 615 620

Tyr Tyr His Gly Gln Thr Glu Gln Cys Val Pro Cys Pro Ala Gly Thr
 625 630 635 640

Phe Gln Glu Arg Glu Gly Gln Leu Ser Cys Asp Leu Cys Pro Gly Ser
 645 650 655

Asp Ala His Gly Pro Leu Gly Ala Thr Asn Val Thr Thr Cys Ala Gly
 660 665 670
 Gln Cys Pro Pro Gly Gln His Ser Val Asp Gly Phe Lys Pro Cys Gln
 675 680 685
 Pro Cys Pro Arg Gly Thr Tyr Gln Pro Glu Ala Gly Arg Thr Leu Cys
 690 695 700
 Phe Pro Cys Gly Gly Leu Thr Thr Lys His Glu Gly Ala Ile Ser
 705 710 715 720
 Phe Gln Asp Cys Asp Thr Lys Val Gln Cys Ser Pro Gly His Tyr Tyr
 725 730 735
 Asn Thr Ser Ile His Arg Cys Ile Arg Cys Ala Met Gly Ser Tyr Gln
 740 745 750
 Pro Asp Phe Arg Gln Asn Phe Cys Ser Arg Cys Pro Gly Asn Thr Ser
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 Thr Asp Phe Asp Gly Ser Thr Ser Val Ala Gln Cys Lys Asn Arg Gln
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 Pro Pro Pro Lys Arg Lys Ile Leu Ile Val Val Pro Glu Ile Phe Leu
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 Pro Ser Glu Asp Glu Cys Gly Asp Val Leu Val Met Arg Lys Asn Ser
 835 840 845
 Ser Pro Ser Ser Ile Thr Thr Tyr Glu Thr Cys Gln Thr Tyr Glu Arg
 850 855 860
 Pro Ile Ala Phe Thr Ala Arg Ser Arg Lys Leu Trp Ile Asn Phe Lys
 865 870 875 880
 Thr Ser Glu Ala Asn Ser Ala Arg Gly Phe Gln Ile Pro Tyr Val Thr
 885 890 895
 Tyr Asp Glu Asp Tyr Glu Gln Leu Val Glu Asp Ile Val Arg Asp Gly
 900 905 910
 Arg Leu Tyr Ala Ser Glu Asn His Gln Glu Ile Leu Lys Asp Lys Lys
 915 920 925
 Leu Ile Lys Ala Phe Phe Glu Val Leu Ala His Pro Gln Asn Tyr Phe
 930 935 940
 Lys Tyr Thr Glu Lys His Lys Glu Met Leu Pro Lys Ser Phe Ile Lys
 945 950 955 960

Leu Leu Arg Ser Lys Val Ser Ser Phe Leu Arg Pro Tyr Lys
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<210> 15
<211> 3177
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: POLYX
CG55096-04

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cattACCAct	tatGAGACCT	gccAGACCTA	cgAGCGTCCC	attGCCTTA	ctgcccGTTc	2820
cagGAAGCTC	tggATCAACT	tcaAGACAAG	cgAGGCCAAC	agcGCCGTG	gttCCAGAT	2880
tccCTATGTT	acctATGATG	aggACTATGA	gcAGCTGGTA	gaAGACATTG	tgCGAGATGG	2940
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gatGCTGCCA	aaATCCTCA	tcaAGCTGCT	ccgCTCCAAA	gttCCAGCT	tcctGAGGCC	3120
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<211> 1009
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: POLYX
CG55096-04

<400> 16
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 20 25 30

Cys Val Glu Gly Thr Asp Asn Cys His Ile Asp Ala Ile Cys Gln Asn
 35 40 45

Thr Pro Arg Ser Tyr Lys Cys Ile Cys Lys Ser Gly Tyr Thr Gly Asp
50 55 60

Gly Lys His Cys Lys Asp Val Asp Glu Cys Glu Arg Glu Asp Asn Ala
65 70 75 80

Gly Cys Val His Asp Cys Val Asn Ile Pro Gly Asn Tyr Arg Cys Thr
85 90 95

Cys Tyr Asp Gly Phe His Leu Ala His Asp Gly His Asn Cys Leu Asp
100 105 110

Val Asp Glu Cys Ala Glu Gly Asn Gly Gly Cys Gln Gln Ser Cys Val
115 120 125

Asn Met Met Gly Ser Tyr Glu Cys His Cys Arg Glu Gly Phe Phe Leu
 130 135 140

Ser Asp Asn Gln His Thr Cys Ile Gln Arg Pro Glu Glu Gly Met Asn
145 150 155 160

Cys Met Asn Lys Asn His Gly Cys Ala His Ile Cys Arg Glu Thr Pro
165 170 175

Asn Gln Arg Asp Cys Lys Leu Thr Cys Asn Tyr Gly Asn Gly Gly Cys
 195 200 205
 Gln His Thr Cys Asp Asp Thr Glu Gln Gly Pro Arg Cys Gly Cys His
 210 215 220
 Ile Lys Phe Val Leu His Thr Asp Gly Lys Thr Cys Ile Gly Glu Arg
 225 230 235 240
 Arg Leu Glu Gln His Ile Pro Thr Gln Ala Val Ser Asn Glu Thr Cys
 245 250 255
 Ala Val Asn Asn Gly Gly Cys Asp Ser Lys Cys His Asp Ala Ala Thr
 260 265 270
 Gly Val His Cys Thr Cys Pro Val Gly Phe Met Leu Gln Pro Asp Arg
 275 280 285
 Lys Thr Cys Lys Asp Ile Asp Glu Cys Arg Leu Asn Asn Gly Gly Cys
 290 295 300
 Asp His Ile Cys Arg Asn Thr Val Gly Ser Phe Glu Cys Ser Cys Lys
 305 310 315 320
 Lys Gly Tyr Lys Leu Leu Ile Asn Glu Arg Asn Cys Gln Asp Ile Asp
 325 330 335
 Glu Arg Ser Phe Asp Arg Thr Cys Asp His Ile Cys Val Asn Thr Pro
 340 345 350
 Gly Ser Phe Gln Cys Leu Cys His Arg Gly Tyr Leu Leu Tyr Gly Ile
 355 360 365
 Thr His Cys Gly Asp Val Asp Glu Cys Ser Ile Asn Arg Gly Gly Cys
 370 375 380
 Arg Phe Gly Cys Ile Asn Thr Pro Gly Ser Tyr Gln Cys Thr Cys Pro
 385 390 395 400
 Ala Gly Gln Gly Arg Leu His Trp Asn Gly Lys Asp Cys Thr Glu Pro
 405 410 415
 Leu Lys Cys Gln Gly Ser Pro Gly Ala Ser Lys Ala Met Leu Ser Cys
 420 425 430
 Asn Arg Ser Gly Lys Asp Thr Cys Ala Leu Thr Cys Pro Ser Arg
 435 440 445
 Ala Arg Phe Leu Pro Glu Ser Gly Asn Gly Phe Thr Val Ser Cys Gly
 450 455 460
 Thr Pro Ser Pro Arg Ala Ala Pro Ala Arg Ala Gly His Asn Gly Asn
 465 470 475 480
 Ser Thr Asn Ser Asn His Cys His Glu Ala Ala Val Leu Ser Ile Lys
 485 490 495

Gln Arg Ala Ser Phe Lys Ile Lys Asp Ala Lys Cys Arg Leu His Leu
 500 505 510

Arg Asn Lys Gly Lys Thr Glu Glu Ala Gly Arg Ile Thr Gly Pro Gly
 515 520 525

Gly Ala Pro Cys Ser Glu Cys Gln Val Thr Phe Ile His Leu Lys Cys
 530 535 540

Asp Ser Ser Arg Lys Gly Lys Gly Arg Arg Ala Arg Thr Pro Pro Gly
 545 550 555 560

Lys Glu Val Thr Arg Leu Thr Leu Glu Leu Glu Ala Glu Val Arg Ala
 565 570 575

Glu Glu Thr Thr Ala Ser Cys Gly Leu Pro Cys Leu Arg Gln Arg Met
 580 585 590

Glu Arg Arg Leu Lys Gly Ser Leu Lys Met Leu Arg Lys Ser Ile Asn
 595 600 605

Gln Asp Arg Phe Leu Leu Arg Leu Ala Gly Leu Asp Tyr Glu Leu Ala
 610 615 620

His Lys Pro Gly Leu Val Ala Gly Glu Arg Ala Glu Pro Met Glu Ser
 625 630 635 640

Cys Arg Pro Gly Gln His Arg Ala Gly Thr Lys Cys Val Ser Cys Pro
 645 650 655

Gln Gly Thr Tyr Tyr His Gly Gln Thr Glu Gln Cys Val Pro Cys Pro
 660 665 670

Ala Gly Thr Phe Gln Glu Arg Glu Gly Gln Leu Ser Cys Asp Leu Cys
 675 680 685

Pro Gly Ser Asp Ala His Gly Pro Leu Gly Ala Thr Asn Val Thr Thr
 690 695 700

Cys Ala Gly Gln Cys Pro Pro Gly Gln His Ser Val Asp Gly Phe Lys
 705 710 715 720

Pro Cys Gln Pro Cys Pro Arg Gly Thr Tyr Gln Pro Glu Ala Gly Arg
 725 730 735

Thr Leu Cys Phe Pro Cys Gly Gly Leu Thr Thr Lys His Glu Gly
 740 745 750

Ala Ile Ser Phe Gln Asp Cys Asp Thr Lys Val Gln Cys Ser Pro Gly
 755 760 765

His Tyr Tyr Asn Thr Ser Ile His Arg Cys Ile Arg Cys Ala Met Gly
 770 775 780

Ser Tyr Gln Pro Asp Phe Arg Gln Asn Phe Cys Ser Arg Cys Pro Gly
 785 790 795 800

Asn Thr Ser Thr Asp Phe Asp Gly Ser Thr Ser Val Ala Gln Cys Lys
 805 810 815

Asn Arg Gln Cys Gly Gly Glu Leu Gly Glu Phe Thr Gly Tyr Ile Glu
 820 825 830

Ser Pro Asn Tyr Pro Gly Asn Tyr Pro Ala Gly Val Glu Cys Ile Trp
 835 840 845

Asn Ile Asn Pro Pro Pro Lys Arg Lys Ile Leu Ile Val Val Pro Glu
 850 855 860

Ile Phe Leu Pro Ser Glu Asp Glu Cys Gly Asp Val Leu Val Met Arg
 865 870 875 880

Lys Asn Ser Ser Pro Ser Ser Ile Thr Thr Tyr Glu Thr Cys Gln Thr
 885 890 895

Tyr Glu Arg Pro Ile Ala Phe Thr Ala Arg Ser Arg Lys Leu Trp Ile
 900 905 910

Asn Phe Lys Thr Ser Glu Ala Asn Ser Ala Arg Gly Phe Gln Ile Pro
 915 920 925

Tyr Val Thr Tyr Asp Glu Asp Tyr Glu Gln Leu Val Glu Asp Ile Val
 930 935 940

Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn His Gln Glu Ile Leu Lys
 945 950 955 960

Asp Lys Lys Leu Ile Lys Ala Phe Phe Glu Val Leu Ala His Pro Gln
 965 970 975

Asn Tyr Phe Lys Tyr Thr Glu Lys His Lys Glu Met Leu Pro Lys Ser
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Phe Ile Lys Leu Leu Arg Ser Lys Val Ser Ser Phe Leu Arg Pro Tyr
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Lys

<210> 17

<211> 1709

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
 10327789.0.16

<400> 17

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<211> 344

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
10327789.0.16

<400> 18

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Cys	Asn	Pro	Gly	Tyr	Lys	Ser	Val	Gly	Ser	Pro	Val	Phe	Val	Cys	Gln
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Ala	Asn	Arg	His	Trp	His	Ser	Glu	Ser	Pro	Leu	Met	Cys	Val	Pro	Leu
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Asp	Cys	Gly	Lys	Pro	Pro	Pro	Ile	Gln	Asn	Gly	Phe	Met	Lys	Gly	Glu
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Asn	Phe	Glu	Val	Gly	Ser	Lys	Val	Gln	Phe	Phe	Cys	Asn	Glu	Gly	Tyr
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Glu	Leu	Val	Gly	Asp	Ser	Ser	Trp	Thr	Cys	Gln	Lys	Ser	Gly	Lys	Trp
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Asn	Lys	Lys	Ser	Asn	Pro	Lys	Cys	Met	Pro	Ala	Lys	Cys	Pro	Glu	Pro
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 Gly Val Val Thr Phe Ser Cys Lys Glu Gly His Val Leu Gln Gly Pro
 145 150 155 160
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 Val Cys Lys Ile Val Leu Cys Thr Pro Pro Pro Leu Ile Ser Phe Gly
 180 185 190
 Val Pro Ile Pro Ser Ser Ala Leu His Phe Gly Ser Thr Val Lys Tyr
 195 200 205
 Ser Cys Val Gly Gly Phe Phe Leu Arg Gly Asn Ser Thr Thr Leu Cys
 210 215 220
 Gln Pro Asp Gly Thr Trp Ser Ser Pro Leu Pro Glu Cys Val Pro Val
 225 230 235 240
 Glu Cys Pro Gln Pro Glu Glu Ile Pro Asn Gly Ile Ile Asp Val Gln
 245 250 255
 Gly Leu Ala Tyr Leu Ser Thr Ala Leu Tyr Thr Cys Lys Pro Gly Phe
 260 265 270
 Glu Leu Val Gly Asn Thr Thr Leu Cys Gly Glu Asn Gly His Trp
 275 280 285
 Leu Gly Gly Lys Pro Thr Cys Lys Ala Ile Glu Cys Leu Lys Pro Lys
 290 295 300
 Glu Ile Leu Asn Gly Lys Phe Ser Tyr Thr Asp Leu His Tyr Gly Gln
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 Thr Val Thr Tyr Ser Cys Asn Arg Gly Phe Arg Leu Glu Gly Ser Gln
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 Cys Leu Asp Leu Phe Arg Asp Arg
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<210> 19
 <211> 1952
 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: POLYX
 10327789.0.140

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 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: POLYX
 10327789.0.140

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 20 25 30

Ala Tyr Ser Cys Asn Lys Gly Phe Tyr Ile Lys Gly Glu Lys Lys Ser
 35 40 45

Thr Cys Glu Ala Thr Gly Gln Trp Ser Ser Pro Ile Pro Thr Cys His
 50 55 60

Pro Val Ser Cys Gly Glu Pro Pro Lys Val Glu Asn Gly Phe Leu Glu
 65 70 75 80

His Thr Thr Gly Arg Ile Phe Glu Ser Glu Val Arg Tyr Gln Cys Asn
 85 90 95

Pro Gly Tyr Lys Ser Val Gly Ser Pro Val Phe Val Cys Gln Ala Asn
 100 105 110
 Arg His Trp His Ser Glu Ser Pro Leu Met Cys Val Pro Leu Asp Cys
 115 120 125
 Gly Lys Pro Pro Pro Ile Gln Asn Gly Phe Met Lys Gly Glu Asn Phe
 130 135 140
 Glu Val Gly Ser Lys Val Gln Phe Phe Cys Asn Glu Gly Tyr Glu Leu
 145 150 155 160
 Val Gly Asp Ser Ser Trp Thr Cys Gln Lys Ser Gly Lys Trp Asn Lys
 165 170 175
 Lys Ser Asn Pro Lys Cys Met Pro Ala Lys Cys Pro Glu Pro Pro Leu
 180 185 190
 Leu Glu Asn Gln Leu Val Leu Lys Glu Leu Thr Thr Glu Val Gly Val
 195 200 205
 Val Thr Phe Ser Cys Lys Glu Gly His Val Leu Gln Gly Pro Ser Val
 210 215 220
 Leu Lys Cys Leu Pro Ser Gln Gln Trp Asn Asp Ser Phe Pro Val Cys
 225 230 235 240
 Lys Ile Val Leu Cys Thr Pro Pro Leu Ile Ser Phe Gly Val Pro
 245 250 255
 Ile Pro Ser Ser Ala Leu His Phe Gly Ser Thr Val Lys Tyr Ser Cys
 260 265 270
 Val Gly Gly Phe Phe Leu Arg Gly Asn Ser Thr Thr Leu Cys Gln Pro
 275 280 285
 Asp Gly Thr Trp Ser Ser Pro Leu Pro Glu Cys Val Pro Val Glu Cys
 290 295 300
 Pro Gln Pro Glu Glu Ile Pro Asn Gly Ile Ile Asp Val Gln Gly Leu
 305 310 315 320
 Ala Tyr Leu Ser Thr Ala Leu Tyr Thr Cys Lys Pro Gly Phe Glu Leu
 325 330 335
 Val Gly Asn Thr Thr Leu Cys Gly Glu Asn Gly His Trp Leu Gly
 340 345 350
 Gly Lys Pro Thr Cys Lys Ala Ile Glu Cys Leu Lys Pro Lys Glu Ile
 355 360 365
 Leu Asn Gly Lys Phe Ser Tyr Thr Asp Leu His Tyr Gly Gln Thr Val
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405

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<210> 21
<211> 6153
<212> DNA
<213> Unknown Organism

<220>
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<223> a, c, t, g, other or unknown

<220>
<223> Description of Unknown Organism: POLYX
      10327789_1

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 <223> Description of Unknown Organism: POLYX
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 35 40 45

Arg Ser Glu Lys Arg Asn Ile Arg Val Gly Val Thr Arg Phe Ser Ser
 50 55 60

Tyr Thr Leu Ala Gly Leu Asp Thr Ile Glu Cys Leu Ala Asp Gly Lys
 65 70 75 80

Trp Ser Arg Ser Asp Gln Gln Cys Leu Ala Val Ser Cys Asp Glu Pro
 85 90 95

Pro Ile Val Asp His Ala Ser Pro Glu Thr Ala His Arg Leu Phe Gly
 100 105 110

Asp Ile Ala Phe Tyr Tyr Cys Ser Asp Gly Tyr Ser Leu Ala Asp Asn
 115 120 125

Ser Gln Leu Leu Cys Asn Ala Gln Gly Lys Trp Val Pro Pro Glu Gly
 130 135 140

Gln Asp Met Pro Arg Cys Ile Ala His Phe Cys Glu Lys Pro Pro Ser
 145 150 155 160

Val Ser Tyr Ser Ile Leu Glu Ser Val Ser Lys Ala Lys Phe Ala Ala
 165 170 175

Gly Ser Val Val Ser Phe Lys Cys Met Glu Gly Phe Val Leu Asn Thr
 180 185 190

Ser Ala Lys Ile Glu Cys Met Arg Gly Gly Gln Trp Asn Pro Ser Pro
 195 200 205
 Met Ser Ile Gln Cys Ile Pro Val Arg Cys Gly Glu Pro Pro Ser Ile
 210 215 220
 Met Asn Gly Tyr Ala Ser Gly Ser Asn Tyr Ser Phe Gly Ala Met Val
 225 230 235 240
 Ala Tyr Ser Cys Asn Lys Gly Phe Tyr Ile Lys Gly Glu Lys Ser
 245 250 255
 Thr Cys Glu Ala Thr Gly Gln Trp Ser Ser Pro Ile Pro Thr Cys His
 260 265 270
 Pro Val Ser Cys Gly Glu Pro Pro Lys Val Glu Asn Gly Phe Leu Glu
 275 280 285
 His Thr Thr Gly Arg Ile Phe Glu Ser Glu Val Arg Tyr Gln Cys Asn
 290 295 300
 Pro Gly Tyr Lys Ser Val Gly Ser Pro Val Phe Val Cys Gln Ala Asn
 305 310 315 320
 Arg His Trp His Ser Glu Ser Pro Leu Met Cys Val Pro Leu Asp Cys
 325 330 335
 Gly Lys Pro Pro Pro Ile Gln Asn Gly Phe Met Lys Gly Glu Asn Phe
 340 345 350
 Glu Val Gly Ser Lys Gly Gln Phe Phe Cys Asn Glu Gly Leu Xaa Ser
 355 360 365
 Phe Val Gly Asp Ser Ser Trp Thr Cys Gln Lys Ser Gly Lys Trp Asn
 370 375 380
 Lys Lys Ser Asn Pro Lys Cys Met Pro Ala Lys Cys Pro Glu Pro Pro
 385 390 395 400
 Leu Leu Glu Asn Gln Leu Val Leu Lys Glu Leu Thr Thr Glu Val Gly
 405 410 415
 Val Val Thr Phe Ser Cys Lys Glu Arg His Val Leu Gln Gly Pro Ser
 420 425 430
 Val Leu Lys Cys Leu Pro Ser Gln Gln Trp Asn Asp Ser Phe Pro Val
 435 440 445
 Cys Lys Ile Val Leu Cys Thr Pro Pro Pro Leu Ile Ser Phe Gly Val
 450 455 460
 Pro Ile Pro Ser Ser Ala Leu His Phe Gly Ser Thr Val Lys Tyr Ser
 465 470 475 480
 Cys Val Gly Gly Phe Phe Leu Arg Gly Asn Ser Thr Thr Leu Cys Gln
 485 490 495

Pro Asp Gly Thr Trp Ser Ser Pro Leu Pro Glu Cys Val Pro Val Glu
 500 505 510

 Cys Pro Gln Pro Glu Glu Ile Pro Asn Gly Ile Ile Asp Val Gln Gly
 515 520 525

 Leu Ala Tyr Leu Ser Thr Ala Leu Tyr Thr Cys Lys Pro Gly Phe Glu
 530 535 540

 Leu Val Gly Asn Thr Thr Leu Cys Gly Glu Asn Gly His Trp Leu
 545 550 555 560

 Gly Gly Lys Pro Thr Cys Lys Ala Ile Glu Cys Leu Lys Pro Lys Glu
 565 570 575

 Ile Leu Asn Gly Lys Phe Ser Tyr Thr Asp Leu His Tyr Gly Gln Thr
 580 585 590

 Val Thr Tyr Ser Cys Asn Arg Gly Phe Arg Leu Glu Gly Pro Ser Ala
 595 600 605

 Leu Thr Cys Leu Glu Thr Gly Asp Trp Asp Val Asp Ala Pro Ser Cys
 610 615 620

 Asn Ala Ile His Cys Asp Ser Pro Gln Pro Ile Glu Asn Gly Phe Val
 625 630 635 640

 Glu Gly Ala Asp Tyr Ser Tyr Gly Ala Ile Ile Ile Tyr Ser Cys Phe
 645 650 655

 Pro Gly Phe Gln Val Ala Gly His Ala Met Gln Thr Cys Glu Glu Ser
 660 665 670

 Gly Trp Ser Ser Ser Ile Pro Thr Cys Met Pro Ile Asp Cys Gly Leu
 675 680 685

 Pro Pro His Ile Asp Phe Gly Asp Cys Thr Lys Leu Lys Asp Asp Gln
 690 695 700

 Gly Tyr Phe Glu Gln Glu Asp Asp Met Met Glu Val Pro Tyr Val Thr
 705 710 715 720

 Pro His Pro Pro Tyr His Leu Gly Ala Val Ala Lys Thr Trp Glu Asn
 725 730 735

 Thr Lys Glu Ser Pro Ala Thr His Ser Ser Asn Phe Leu Tyr Gly Thr
 740 745 750

 Met Val Ser Tyr Thr Cys Asn Pro Gly Tyr Glu Leu Leu Gly Asn Pro
 755 760 765

 Val Leu Ile Cys Gln Glu Asp Gly Thr Trp Asn Gly Ser Ala Pro Ser
 770 775 780

 Cys Ile Ser Ile Glu Cys Asp Leu Pro Thr Ala Pro Glu Asn Gly Phe
 785 790 795 800

Leu Arg Phe Thr Glu Thr Ser Met Gly Ser Ala Val Gln Tyr Ser Cys
 805 810 815

 Lys Pro Gly His Ile Leu Ala Gly Ser Asp Leu Arg Leu Cys Leu Glu
 820 825 830

 Asn Arg Lys Trp Ser Gly Ala Ser Pro Arg Cys Glu Ala Ile Ser Cys
 835 840 845

 Lys Lys Pro Asn Pro Val Met Asn Gly Ser Ile Lys Gly Ser Asn Tyr
 850 855 860

 Thr Tyr Leu Ser Thr Leu Tyr Tyr Glu Cys Asp Pro Gly Tyr Val Leu
 865 870 875 880

 Asn Gly Thr Glu Arg Arg Thr Cys Gln Asp Asp Lys Asn Trp Asp Glu
 885 890 895

 Asp Glu Pro Ile Cys Ile Pro Val Asp Cys Ser Ser Pro Pro Val Ser
 900 905 910

 Ala Asn Gly Gln Val Arg Gly Asp Glu Tyr Thr Phe Gln Lys Glu Ile
 915 920 925

 Glu Tyr Thr Cys Asn Glu Gly Phe Leu Leu Glu Gly Ala Arg Ser Arg
 930 935 940

 Val Cys Leu Ala Asn Gly Ser Trp Ser Gly Ala Thr Pro Asp Cys Val
 945 950 955 960

 Pro Val Arg Cys Ala Thr Pro Pro Gln Leu Ala Asn Gly Val Thr Glu
 965 970 975

 Gly Leu Asp Tyr Gly Phe Met Lys Glu Val Thr Phe His Cys His Glu
 980 985 990

 Gly Tyr Ile Leu His Gly Ala Pro Lys Leu Thr Cys Gln Ser Asp Gly
 995 1000 1005

 Asn Trp Asp Ala Glu Ile Pro Leu Cys Lys Pro Val Asn Cys Gly Pro
 1010 1015 1020

 Pro Glu Asp Leu Ala His Gly Phe Pro Asn Gly Phe Ser Phe Ile His
 1025 1030 1035 1040

 Gly Gly His Ile Gln Tyr Gln Cys Phe Pro Gly Tyr Lys Leu His Gly
 1045 1050 1055

 Asn Ser Ser Arg Arg Cys Leu Ser Asn Gly Ser Trp Ser Gly Ser Ser
 1060 1065 1070

 Pro Ser Cys Leu Pro Cys Arg Cys Ser Thr Pro Val Ile Glu Tyr Gly
 1075 1080 1085

 Thr Val Asn Gly Thr Asp Phe Asp Cys Gly Lys Ala Ala Arg Ile Gln
 1090 1095 1100

Cys Phe Lys Gly Phe Lys Leu Leu Gly Leu Ser Glu Ile Thr Cys Glu
 1105 1110 1115 1120
 Ala Asp Gly Gln Trp Ser Ser Gly Phe Pro His Cys Glu His Thr Ser
 1125 1130 1135
 Cys Gly Ser Leu Pro Met Ile Pro Asn Ala Phe Ile Ser Glu Thr Ser
 1140 1145 1150
 Ser Trp Lys Glu Asn Val Ile Thr Tyr Ser Cys Arg Ser Gly Tyr Val
 1155 1160 1165
 Ile Gln Gly Ser Ser Asp Leu Ile Cys Thr Glu Lys Gly Val Trp Ser
 1170 1175 1180
 Gln Pro Tyr Pro Val Cys Glu Pro Leu Ser Cys Gly Ser Pro Pro Ser
 1185 1190 1195 1200
 Val Ala Asn Ala Val Ala Thr Gly Glu Ala His Thr Tyr Glu Ser Glu
 1205 1210 1215
 Val Lys Leu Arg Cys Leu Glu Gly Tyr Thr Met Asp Thr Asp Thr Asp
 1220 1225 1230
 Thr Phe Thr Cys Gln Lys Asp Gly Arg Trp Phe Pro Glu Arg Ile Ser
 1235 1240 1245
 Cys Ser Pro Lys Lys Cys Pro Leu Pro Glu Asn Ile Thr His Ile Leu
 1250 1255 1260
 Val His Gly Asp Asp Phe Ser Val Asn Arg Gln Val Ser Val Ser Cys
 1265 1270 1275 1280
 Ala Glu Gly Tyr Thr Phe Glu Gly Val Asn Ile Ser Val Cys Gln Leu
 1285 1290 1295
 Asp Gly Thr Trp Glu Pro Pro Phe Ser Asp Glu Ser Cys Ser Pro Val
 1300 1305 1310
 Ser Cys Gly Lys Pro Glu Ser Pro Glu His Gly Phe Val Val Gly Ser
 1315 1320 1325
 Lys Tyr Thr Phe Glu Ser Thr Ile Ile Tyr Gln Cys Glu Pro Gly Tyr
 1330 1335 1340
 Glu Leu Glu Asn Leu Ala Val Asn Pro Ser Gly Pro Gly Leu Phe Leu
 1345 1350 1355 1360
 Val Asp Arg Thr Leu Ser Cys Arg Ser Glu Leu Ala Arg Gly Pro Ile
 1365 1370 1375
 Gln Thr Leu Phe Ala Trp Val Ser Ala Ala Glu Gly Ala Glu Gln Arg
 1380 1385 1390
 Ile Leu Val Asn Arg Lys Cys Cys Cys Leu Ile Ile Pro Leu Glu Val
 1395 1400 1405

Leu Ser Gln Arg Asn Thr Arg Pro Cys Glu Val Ser Val Arg Pro Tyr
 1410 1415 1420

 Trp Gly Gly Asn Arg Glu Arg Val Cys Gln Glu Asn Arg Gln Trp Ser
 1425 1430 1435 1440

 Gly Gly Val Ala Ile Cys Lys Glu Thr Arg Cys Glu Thr Pro Leu Glu
 1445 1450 1455

 Phe Leu Asn Gly Lys Ala Asp Ile Glu Asn Arg Thr Thr Gly Pro Asn
 1460 1465 1470

 Val Val Tyr Ser Cys Asn Arg Gly Tyr Ser Leu Glu Gly Pro Ser Glu
 1475 1480 1485

 Ala His Cys Thr Glu Asn Gly Thr Trp Ser His Pro Val Pro Leu Cys
 1490 1495 1500

 Lys Pro Asn Pro Cys Pro Val Pro Phe Val Ile Pro Glu Asn Ala Leu
 1505 1510 1515 1520

 Leu Ser Glu Lys Glu Phe Tyr Val Asp Gln Asn Val Ser Ile Lys Cys
 1525 1530 1535

 Arg Glu Gly Phe Leu Leu Gln Gly His Gly Ile Ile Thr Cys Asn Pro
 1540 1545 1550

 Asp Glu Thr Trp Thr Gln Thr Ser Ala Lys Cys Glu Arg Arg Tyr Thr
 1555 1560 1565

 Gln Gln Pro Lys Ser Leu Asn Phe Gln Leu Ala Ala Tyr Cys Ser Ile
 1570 1575 1580

 Arg Met Phe Ile Leu Arg Gly Val Gln Asp Gly Gln Leu Glu Thr
 1585 1590 1595 1600

 Ala Val Ala Gly Ala Ser His Arg Glu Glu Gln Lys Gln Lys Arg Glu
 1605 1610 1615

 Lys Ala Arg Trp Tyr Asn Gly Pro Pro Gly Ser His Met Gly Gln Ala
 1620 1625 1630

 Glu Leu Pro Pro Ala Lys Gly Gly Pro Pro Cys Gly Asn Phe
 1635 1640 1645

 Ser Asn Ser Ser Gln Gly Phe Met Asn Arg Pro Leu Ile Ser Leu Arg
 1650 1655 1660

 Trp Ser Pro Trp Gly Ser Met Trp Pro Trp Ser Pro Gln Ile Ser Arg
 1665 1670 1675 1680

 Leu Ser Pro Ser Pro Ala Gly Ser Glu Glu Ser Arg Gln Ala Gly Leu
 1685 1690 1695

 Val Gly Phe Pro Thr Ala Gln Phe Thr Cys Ser Ala Lys Gly Gln Leu
 1700 1705 1710

Glu Arg Phe Val Lys Arg Val Pro Asp Pro Met Pro Pro Asp Trp Asp
 1715 1720 1725

Glu Thr Pro Pro Gln Gln Gly Ser Arg Met Arg Pro Pro His Asn Arg
 1730 1735 1740

Gly His Gln Thr Pro Tyr Thr Arg Val Phe Leu Leu Ala Ser Gly Gln
 1745 1750 1755 1760

Cys Pro Ser Gly Thr Glu Leu Pro Glu Glu Arg Ala Gly Ser His Leu
 1765 1770 1775

Cys Cys Ser Ala Ala Ser Ala Gly Lys Ala Gln Asn Trp Ala Glu Ala
 1780 1785 1790

Arg Ile Asp Glu Leu Lys Glu Val Gly Phe Arg Lys Trp Val Ile Met
 1795 1800 1805

Lys Phe Ala Glu Leu Lys Glu His Val Leu Asn Gln Cys Lys Asp Ala
 1810 1815 1820

Lys Asn Gln Asp Lys Thr Leu Gln Asp Pro Leu Thr Arg Ile Thr Ser
 1825 1830 1835 1840

Leu Glu Arg Asn Val Asn Asp Leu Met Glu Leu Lys Asn Thr Thr Arg
 1845 1850 1855

Glu Leu His Asn Ala Thr Thr Lys Gln Gly Gln His Ser Ser Ser Gly
 1860 1865 1870

Asn Pro Glu Asn Pro Ser Lys Ile Leu His Glu Lys Ile Asn Pro Lys
 1875 1880 1885

Thr His Asn Pro Gln Val Leu Gln Glu Ile Ser Cys Gly Pro Pro Ala
 1890 1895 1900

His Val Glu Asn Ala Ile Ala Arg Gly Val His Tyr Gln Tyr Gly Asp
 1905 1910 1915 1920

Met Ile Thr Tyr Ser Cys Tyr Ser Gly Tyr Met Leu Glu Gly Phe Leu
 1925 1930 1935

Arg Ser Val Cys Leu Glu Asn Gly Thr Trp Thr Ser Pro Pro Ile Cys
 1940 1945 1950

Arg Ala Val Cys Arg Phe Pro Cys Gln Asn Gly Ile Cys Gln Arg
 1955 1960 1965

Pro Asn Ala Cys Ser Cys Pro Glu Gly Trp Met Gly Arg Leu Cys Glu
 1970 1975 1980

Glu Pro Ile Cys Ile Leu Pro Cys Leu Asn Gly Gly Arg Cys Val Ala
 1985 1990 1995 2000

Pro Tyr Gln Cys Asp Cys Pro Pro Gly Trp Thr Gly Ser Arg Cys His
 2005 2010 2015

Thr Gly Arg Pro Leu Ser Trp Phe Val Phe Leu Val Ala Gln Ala His
 2020 2025 2030

Glu Thr Pro Glu Asp Ile Glu Glu Cys Asp Leu Asp Ser Glu Val Val
 2035 2040 2045

Ala Lys
 2050

<210> 23
<211> 2216
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: POLYX
AC016030_A.0.82

<400> 23
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aggagcccg ggcgcctctcg ccgcctccccg cgccgcccgtc cgcacctccc caccgcccgc 180
cgccccgcgc cggccgccccg caaagcatga gtgagccgc tctctgcagc tgcccggggc 240
gcgaatggca ggctgttcc gcggagtaaa aggtggccgc ggtcagtgg ctgtttccaat 300
gacggacatt aaccagactg tcagatcctg gggagtcgcg agccccgagt ttggagttt 360
ttccccccac aacgtcacag tccgaactgc agagggaaag gaaggccgca ggaaggcgaa 420
gctcggggtc cggcacgtag ttgggaaact tgcgggtcct agaagtcgcc tccccgcctt 480
gccggccgccc cttgcagccc cgagccgagc agcaaagtga gacattgtgc gcctgccaga 540
tccgcccggcc gcggaccggg gctgcctcg aaacacagag gggcttctc tcgcccgtca 600
tataatttagc ctgcacacaa agggagcagc tgaatggagg ttgtcactct ctggaaaagg 660
atttctgacc gagcgttcc aatggacatt ctccagtc tctggaaaga ttctcgctaa 720
tggatttcct gctgctcggt ctctgtctat actggctgtc gaggaggccc tcgggggtgg 780
tcttgtgtct gctggggggc tgctttcaga tgctgcccgc cgcccccagc gggtgccgc 840
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gcgcgggcca gttcacgggg ttaatgcagc tcacgtggcctatctggat cacaatcaca 1020
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gtgcctaccg gagctgcggc ggcgtctcca cacgcaacca tgaagttgaa ggacacaaaa 1140
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aaatggaaagg aaatggacag atggatgact tgggtgtc ttgaggaattt acagattacc 1260
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aaaagatcaa gttgaagaaa agtaaaaatg tagcaactga aggaaccagt acccagaaag 1440
aatttgaagt gaaagatcct gagctggagg cccagggaga tgacatggtt tgtgatgatc 1500
cgaggcgtgg ggagatgaca tcagaaaacc tggtccaaac tgctccaaaa aagaagaaaa 1560
ataaaagggaa aaaagggttg ggccttctc agagcactgc tgccaaagggtg cccaaaaaaag 1620
cgaagacatg gattcctgaa gttcatgatc agaaagcaga tgtgtcagct tggaaggacc 1680
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caatccaagc cctgacccgtt gcacccgtca tccgtgaccaa actggacatc cttggggctg 1800
ctgagacagg aagtggaaa actcttcct ttgccttccc aatgattcat gcggtgtgc 1860
agtggcagaa gaggaaatgct gcccctccctc caagtaacac cgaagcaca cctggagaga 1920
ccagaactga ggccggagct gagacttagat taccaggcaa ggctgaagct gagtctgatg 1980
cattgcgttca cgatactgtt attgagagtg aagcactgccc cagtgatatt gcagccgagg 2040
ccagagccaa gactggaggc actgtctcag accaggcggt gctctttgag tgacgtatgat 2100
gctgggtgaag ggccttcttcc cctgatcagg gagaacacgtt ttcccaaaca gaatggaaat 2160
gaagaggaaa atctttgata agagcagact ggaagtctaa aacaggagtt ggtatga 2216

<210> 24

<211> 457

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX

AC016030_A.0.82

<400> 24

Met Asp Phe Leu Leu Leu Gly Leu Cys Leu Tyr Trp Leu Leu Arg Arg
1 5 10 15

Pro Ser Gly Val Val Leu Cys Leu Leu Gly Ala Cys Phe Gln Met Leu
20 25 30

Pro Ala Ala Pro Ser Gly Cys Pro Gln Leu Cys Arg Cys Glu Gly Arg
35 40 45

Leu Leu Tyr Cys Glu Ala Leu Asn Leu Thr Glu Ala Pro His Asn Leu
50 55 60

Ser Gly Leu Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Ser Glu Leu
65 70 75 80

Arg Ala Gly Gln Phe Thr Gly Leu Met Gln Leu Thr Trp Leu Tyr Leu
85 90 95

Asp His Asn His Ile Cys Ser Val Gln Gly Asp Ala Phe Gln Lys Leu
100 105 110

Arg Arg Val Lys Glu Leu Thr Leu Ser Ala Tyr Arg Ser Cys Gly Gly
115 120 125

Val Ser Thr Arg Asn His Glu Val Glu Gly His Lys Ile Lys Ala Lys
130 135 140

Ala Val Lys Leu Trp Gln Ile Ser Asp Lys Gly Asn Gln Ser Cys Gly
145 150 155 160

Lys Met Glu Gly Asn Gly Gln Met Asp Asp Leu Val Cys Phe Glu Glu
165 170 175

Leu Thr Asp Tyr Gln Leu Val Ser Pro Ala Lys Asn Pro Ser Ser Leu
180 185 190

Phe Ser Lys Glu Ala Pro Lys Arg Lys Ala Gln Ala Val Ser Glu Glu
195 200 205

Glu Glu Glu Glu Gly Lys Ser Ser Ser Pro Lys Lys Lys Ile Lys
210 215 220

Leu Lys Lys Ser Lys Asn Val Ala Thr Glu Gly Thr Ser Thr Gln Lys
225 230 235 240

Glu Phe Glu Val Lys Asp Pro Glu Leu Glu Ala Gln Gly Asp Asp Met
245 250 255

Val Cys Asp Asp Pro Glu Ala Gly Glu Met Thr Ser Glu Asn Leu Val
 260 265 270

Gln Thr Ala Pro Lys Lys Lys Asn Lys Gly Lys Lys Gly Leu Glu
 275 280 285

Pro Ser Gln Ser Thr Ala Ala Lys Val Pro Lys Lys Ala Lys Thr Trp
 290 295 300

Ile Pro Glu Val His Asp Gln Lys Ala Asp Val Ser Ala Trp Lys Asp
 305 310 315 320

Leu Phe Val Pro Arg Pro Val Leu Arg Ala Leu Ser Phe Leu Gly Phe
 325 330 335

Ser Ala Pro Thr Pro Ile Gln Ala Leu Thr Leu Ala Pro Ala Ile Arg
 340 345 350

Asp Lys Leu Asp Ile Leu Gly Ala Ala Glu Thr Gly Ser Gly Lys Thr
 355 360 365

Leu Ala Phe Ala Ile Pro Met Ile His Ala Val Leu Gln Trp Gln Lys
 370 375 380

Arg Asn Ala Ala Pro Pro Pro Ser Asn Thr Glu Ala Pro Pro Gly Glu
 385 390 395 400

Thr Arg Thr Glu Ala Gly Ala Glu Thr Arg Leu Pro Gly Lys Ala Glu
 405 410 415

Ala Glu Ser Asp Ala Leu Pro Asp Asp Thr Val Ile Glu Ser Glu Ala
 420 425 430

Leu Pro Ser Asp Ile Ala Ala Glu Ala Arg Ala Lys Thr Gly Gly Thr
 435 440 445

Val Ser Asp Gln Ala Leu Leu Phe Glu
 450 455

<210> 25

<211> 921

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
 h_nh0443k08_A

<400> 25

atggcgaaga ttgagaaaaa cgctcccacg atggaaaaaa agccagaact gtttaacatc 60
 atggaagtag atggagtccc tacgttgata ttatcaaaag aatggtgaaa aaaagtatgt 120
 aatttccaag ccaaggctga tcatcttatt ctggcaacct acccaaagtc aggtacaaca 180
 tggatgcatg aaatttttaga catgattcta aatgatggtg atgtggagaa atgcaaaaga 240
 gcccagactc tagatagaca cgcttcctt gaactgaaat ttccccataa agaaaaacca 300
 gatttggagt tcgttcttga aatgtcctca ccacaactga taaaaacaca tctcccttca 360
 catctgatcc caccatctat ctggaaagaa aactgcaaga ttgtctatgt ggccagaaat 420

cccaaggatt gcctgggtgc ctactaccac tttcacagga tggcttcctt tatgcctgat 480
 cctcagaact tagaggaatt ttatgagaaa ttcatgtccg gaaaagggtga gttcggttcc 540
 tggtttgacc atgtgaaagg atggtgggct gcaaaaagaca tgcaccggat cctctacctc 600
 ttctacgagg atattaaaca gaatccaaaa catgagatcc acaaggtgtt ggaattcttg 660
 gagaaaaactt ggtcaggta tggtataaac aagattgtcc accatacctc atttgatgta 720
 atgaaggata atcccatggc caaccatact gcgttacctg ctcacatatt caatcactcc 780
 atctcaaaat ttatgagaa aggtggatg cctggagact ggaagaacca ctttactgtg 840
 gctttgaatg agaacttga taagcattat gaaaagaaga tggcagggtc cacactgaac 900
 ttctgcctgg agatctgaga 9 921

<210> 26

<211> 305

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
 h_nh0443k08_A

<400> 26

Met Ala Lys Ile Glu Lys Asn Ala Pro Thr Met Glu Lys Lys Pro Glu
 1 5 10 15Leu Phe Asn Ile Met Glu Val Asp Gly Val Pro Thr Leu Ile Leu Ser
 20 25 30Lys Glu Trp Trp Glu Lys Val Cys Asn Phe Gln Ala Lys Pro Asp Asp
 35 40 45Leu Ile Leu Ala Thr Tyr Pro Lys Ser Gly Thr Thr Trp Met His Glu
 50 55 60Ile Leu Asp Met Ile Leu Asn Asp Gly Asp Val Glu Lys Cys Lys Arg
 65 70 75 80Ala Gln Thr Leu Asp Arg His Ala Phe Leu Glu Leu Lys Phe Pro His
 85 90 95Lys Glu Lys Pro Asp Leu Glu Phe Val Leu Glu Met Ser Ser Pro Gln
 100 105 110Leu Ile Lys Thr His Leu Pro Ser His Leu Ile Pro Pro Ser Ile Trp
 115 120 125Lys Glu Asn Cys Lys Ile Val Tyr Val Ala Arg Asn Pro Lys Asp Cys
 130 135 140Leu Val Ser Tyr Tyr His Phe His Arg Met Ala Ser Phe Met Pro Asp
 145 150 155 160Pro Gln Asn Leu Glu Glu Phe Tyr Glu Lys Phe Met Ser Gly Lys Gly
 165 170 175Glu Phe Gly Ser Trp Phe Asp His Val Lys Gly Trp Trp Ala Ala Lys
 180 185 190

Asp Met His Arg Ile Leu Tyr Leu Phe Tyr Glu Asp Ile Lys Gln Asn
 195 200 205

Pro Lys His Glu Ile His Lys Val Leu Glu Phe Leu Glu Lys Thr Trp
 210 215 220

Ser Gly Asp Val Ile Asn Lys Ile Val His His Thr Ser Phe Asp Val
 225 230 235 240

Met Lys Asp Asn Pro Met Ala Asn His Thr Ala Val Pro Ala His Ile
 245 250 255

Phe Asn His Ser Ile Ser Lys Phe Met Arg Lys Gly Gly Met Pro Gly
 260 265 270

Asp Trp Lys Asn His Phe Thr Val Ala Leu Asn Glu Asn Phe Asp Lys
 275 280 285

His Tyr Glu Lys Lys Met Ala Gly Ser Thr Leu Asn Phe Cys Leu Glu
 290 295 300

Ile
 305

<210> 27
<211> 893
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: POLYX
 h_nh0778p17_A

<400> 27
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tatttatgaa agagagcctg tagctgagag acacctacat gaaatccaaa aactacagga 180
aagtattaac aatttggcag ataatgttca aaaatttggg cagcaacaga aaagtcttgt 240
ggcttcaatg agaagggtta gtctactta gagagaggtt accattacaa aggagataaa 300
aattcaggca gaatacatca acagaagttt gaatgattt gttaaaaagtc 360
agaggttgaa aatggtccat cttcagtggc cacaaggata cttaaatctc agcatgctgc 420
aatgttccgc cattttcagc aaatcatgtt tatataacaat gacacaatag cagcaaagca 480
agagaagtgc aagacattta ttttacgtca gcttgaagtt gctggaaaag agatgtctga 540
agaagatgta aatgatatgc ttcatcaagg aaaatggaa gtttttaatg aaagcttact 600
tacagaaatc aatatcacta aagcacaact ttcaagatggtta gaaacagagac acaaggaact 660
tgttaatttgg gagaacaaa taaaggattt aagggttccat ttcattcaga tatctcttt 720
agttagaggaa caaggagaga gcatcaacaa tattgaaatg acagtgaata gtacaaaaga 780
gtatgttaac aatactaaag agaaatttgg actagctgtt aaataaaaaaa aaagaaaatcc 840
ttgcagagta ctgtgttgc ggtgctgtcc atgctgttagc tcaaaaataaa gaa 893

<210> 28
<211> 294
<212> PRT
<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
h_nh0778p17_A

<400> 28

Met Lys Asp Arg Leu Gln Glu Leu Lys Gln Arg Thr Lys Glu Ile Glu
1 5 10 15Leu Ser Arg Asp Ser His Val Ser Thr Thr Glu Thr Glu Glu Gln Gly
20 25 30Val Phe Leu Gln Gln Ala Val Ile Tyr Glu Arg Glu Pro Val Ala Glu
35 40 45Arg His Leu His Glu Ile Gln Lys Leu Gln Glu Ser Ile Asn Asn Leu
50 55 60Ala Asp Asn Val Gln Lys Phe Gly Gln Gln Lys Ser Leu Val Ala
65 70 75 80Ser Met Arg Arg Phe Ser Leu Leu Lys Arg Glu Ser Thr Ile Thr Lys
85 90 95Glu Ile Lys Ile Gln Ala Glu Tyr Ile Asn Arg Ser Leu Asn Asp Leu
100 105 110Val Lys Glu Val Lys Ser Glu Val Glu Asn Gly Pro Ser Ser Val
115 120 125Val Thr Arg Ile Leu Lys Ser Gln His Ala Ala Met Phe Arg His Phe
130 135 140Gln Gln Ile Met Phe Ile Tyr Asn Asp Thr Ile Ala Ala Lys Gln Glu
145 150 155 160Lys Cys Lys Thr Phe Ile Leu Arg Gln Leu Glu Val Ala Gly Lys Glu
165 170 175Met Ser Glu Glu Asp Val Asn Asp Met Leu His Gln Gly Lys Trp Glu
180 185 190Val Phe Asn Glu Ser Leu Leu Thr Glu Ile Asn Ile Thr Lys Ala Gln
195 200 205Leu Ser Glu Ile Glu Gln Arg His Lys Glu Leu Val Asn Leu Glu Asn
210 215 220Gln Ile Lys Asp Leu Arg Asp Leu Phe Ile Gln Ile Ser Leu Leu Val
225 230 235 240Glu Glu Gln Gly Glu Ser Ile Asn Asn Ile Glu Met Thr Val Asn Ser
245 250 255Thr Lys Glu Tyr Val Asn Asn Thr Lys Glu Lys Phe Gly Leu Ala Val
260 265 270Lys Tyr Lys Lys Arg Asn Pro Cys Arg Val Leu Cys Cys Trp Cys Cys
275 280 285

Pro Cys Cys Ser Ser Lys
290

<210> 29
<211> 892
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: POLYX
hhn0778p17_A1

<400> 29
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gacagtcatg tatcaactac agaaacagag gaacaagggg tgtttctaca gcaagctgtt 120
atttatgaaa gagagcctgt agctgagaga cacctacatg aaatccaaaa actacaggaa 180
agtattaaca atttggcaga taatgttcaa aaatttgggc agcaacagaa aagtctggtg 240
gcttcaatga gaagggttag tctacttaag agagagtcta ccattacaaa ggagataaaa 300
attcaggcag aatacatcaa cagaagttt aatgatttag ttaaagaagt taaaaagtca 360
gaggttgaaa atggtccatc ttcatgtggc acaaggatc ttaaatctca gcatgctgca 420
atgttccgcc atttcagca aatcatgtt atatacaatg acacaatagc agcaaagcaa 480
gagaagtgcg agacattt tttacgtcg cttgaagttt ctggaaaaga gatgtctgaa 540
gaagatgtaa atgatatgct tcatacgaa aaatggaaag ttttaatga aagcttactt 600
acagaaatca atatcaacta agcacaactt tcagagattt aacagagaca caaggaactt 660
gttaatttgg agaacccaaat aaaggattt agggatctt tcattcagat atctcttta 720
gttagaggaac aaggagagag catcaacaat attgaaatga cagtgaatag tacaaaagag 780
tatgttaaca atactaaaga gaaatttggc ctatgttcaa aataaaaaa aagaaatcct 840
tgcagagtac tgttgttgc tgctgtcca tgctgttagct caaaataaag aa 892

<210> 30
<211> 294
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: POLYX
hhn0778p17_A1

<400> 30
Met Lys Asp Arg Leu Gln Glu Leu Lys Gln Arg Thr Lys Glu Ile Glu
1 5 10 15

Leu Ser Arg Asp Ser His Val Ser Thr Thr Glu Glu Gln Gly
20 25 30

Val Phe Leu Gln Gln Ala Val Ile Tyr Glu Arg Glu Pro Val Ala Glu
35 40 45

Arg His Leu His Glu Ile Gln Lys Leu Gln Glu Ser Ile Asn Asn Leu
50 55 60

Ala Asp Asn Val Gln Lys Phe Gly Gln Gln Lys Ser Leu Val Ala
65 70 75 80

Ser Met Arg Arg Phe Ser Leu Leu Lys Arg Glu Ser Thr Ile Thr Lys
 85 90 95

Glu Ile Lys Ile Gln Ala Glu Tyr Ile Asn Arg Ser Leu Asn Asp Leu
 100 105 110

Val Lys Glu Val Lys Lys Ser Glu Val Glu Asn Gly Pro Ser Ser Val
 115 120 125

Val Thr Arg Ile Leu Lys Ser Gln His Ala Ala Met Phe Arg His Phe
 130 135 140

Gln Gln Ile Met Phe Ile Tyr Asn Asp Thr Ile Ala Ala Lys Gln Glu
 145 150 155 160

Lys Cys Lys Thr Phe Ile Leu Arg Gln Leu Glu Val Ala Gly Lys Glu
 165 170 175

Met Ser Glu Glu Asp Val Asn Asp Met Leu His Gln Gly Lys Trp Glu
 180 185 190

Val Phe Asn Glu Ser Leu Leu Thr Glu Ile Asn Ile Thr Lys Ala Gln
 195 200 205

Leu Ser Glu Ile Glu Gln Arg His Lys Glu Leu Val Asn Leu Glu Asn
 210 215 220

Gln Ile Lys Asp Leu Arg Asp Leu Phe Ile Gln Ile Ser Leu Leu Val
 225 230 235 240

Glu Glu Gln Gly Glu Ser Ile Asn Asn Ile Glu Met Thr Val Asn Ser
 245 250 255

Thr Lys Glu Tyr Val Asn Asn Thr Lys Glu Lys Phe Gly Leu Ala Val
 260 265 270

Lys Tyr Lys Lys Arg Asn Pro Cys Arg Val Leu Cys Cys Trp Cys Cys
 275 280 285

Pro Cys Cys Ser Ser Lys
 290

<210> 31

<211> 892

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
 CG55655_02

<400> 31

aagatgaaag accgacttca agaactaaag cagagaacaa agggaaattga actctctaga 60
 gacagtcatg tatcaactac agaaaacagag gaacaagggg tggttctaca gcaagctgtt 120
 atttatgaaa gagagcctgt agctgagaga cacctacatg aaatccaaaa actacagcaa 180
 agtattaaca atttggcaga taatgttcaa aaatttgggc agcaacagaa aagtctgtg 240
 gcttcaatga gaaggtttag tctacttaag agagagtcta ccattacaaa ggagataaaa 300

attcaggcag aatacatcaa cagaagtttgc aatgatggtag ttaaagaagt taaaaagtca 360
 gaggttgaaa atggccatc ttcagtggtc acaaggatac ttaaaatctca gcatgctgca 420
 atgttccgcc attttcagca aatcatgttt atatacaatg acacaatagc agcaaagcaa 480
 gagaagtgcgca agacatttat ttacgtcgat cttgaagttt ctggaaaaga gatgtctgaa 540
 gaagatgtaa atgatatgct tcatacgaggaa aaatgggaag ttttaatga aagcttactt 600
 acagaaatca atatcactaa agcacaactt tcagagattt aacagagaca caaggaactt 660
 gttaattttgg agaaccat aaaggattt agggatctt tcattcagat atctcttta 720
 gtagaggaac aaggagagag catcaacaat attgaaatga cagtgaatag tacaagag 780
 tatgttaaca atactaaaga gaaatttggc ctatgtttaa aataaaaaa aagaaatcct 840
 tgcagagttac tgtgttggc tgctgtccca tgctgttagt caaaataaag aa 892

<210> 32

<211> 294

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
 CG55655_02

<400> 32

Met	Lys	Asp	Arg	Leu	Gln	Glu	Leu	Lys	Gln	Arg	Thr	Lys	Glu	Ile	Glu
1				5				10					15		

Leu	Ser	Arg	Asp	Ser	His	Val	Ser	Thr	Thr	Glu	Thr	Glu	Gln	Gly
						20		25				30		

Val	Phe	Leu	Gln	Gln	Ala	Val	Ile	Tyr	Glu	Arg	Glu	Pro	Val	Ala	Glu
						35		40				45			

Arg	His	Leu	His	Glu	Ile	Gln	Lys	Leu	Gln	Glu	Ser	Ile	Asn	Asn	Leu
						50		55			60				

Ala	Asp	Asn	Val	Gln	Lys	Phe	Gly	Gln	Gln	Lys	Ser	Leu	Val	Ala
						65		70		75		80		

Ser	Met	Arg	Arg	Phe	Ser	Leu	Leu	Lys	Arg	Glu	Ser	Thr	Ile	Thr	Lys
						85		90				95			

Glu	Ile	Lys	Ile	Gln	Ala	Glu	Tyr	Ile	Asn	Arg	Ser	Leu	Asn	Asp	Leu
						100		105				110			

Val	Lys	Glu	Val	Lys	Ser	Glu	Val	Glu	Asn	Gly	Pro	Ser	Ser	Val
						115		120			125			

Val	Thr	Arg	Ile	Leu	Lys	Ser	Gln	His	Ala	Ala	Met	Phe	Arg	His	Phe
						130		135			140				

Gln	Gln	Ile	Met	Phe	Ile	Tyr	Asn	Asp	Thr	Ile	Ala	Ala	Lys	Gln	Glu
						145		150		155			160		

Lys	Cys	Lys	Thr	Phe	Ile	Leu	Arg	Gln	Leu	Glu	Val	Ala	Gly	Lys	Glu
						165		170			175				

Met	Ser	Glu	Glu	Asp	Val	Asn	Asp	Met	Leu	His	Gln	Gly	Lys	Trp	Glu
						180		185			190				

Val Phe Asn Glu Ser Leu Leu Thr Glu Ile Asn Ile Thr Lys Ala Gln
 195 200 205

Leu Ser Glu Ile Glu Gln Arg His Lys Glu Leu Val Asn Leu Glu Asn
 210 215 220

Gln Ile Lys Asp Leu Arg Asp Leu Phe Ile Gln Ile Ser Leu Leu Val
 225 230 235 240

Glu Glu Gln Gly Glu Ser Ile Asn Asn Ile Glu Met Thr Val Asn Ser
 245 250 255

Thr Lys Glu Tyr Val Asn Asn Thr Lys Glu Lys Phe Gly Leu Ala Val
 260 265 270

Lys Tyr Lys Lys Arg Asn Pro Cys Arg Val Leu Cys Cys Trp Cys Cys
 275 280 285

Pro Cys Cys Ser Ser Lys
 290

<210> 33

<211> 967

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
 GM_11817402_A

<400> 33

tcatggaaatca atgataaaagg gacggaattc atgtgggggg ttggagtgga cgcaggcg 60
 agtgggtcca gcagatggaa acacagctgc caagtctgcc cctgtcctta gcttctgcag 120
 gaggtgtggg gaactctgcc ttctacaatg tgatgctgca cagagagctg tctgtcatct 180
 tcgaccaatt ccatggcatt caggacactg tgatagggga aggaacgcac tttctcatcc 240
 catggaaaaa gaaaccaatt attttgact gctgctctcg accacattat gcaccaatca 300
 tcactgtgag caaagattgt caccatgtca ccatcacact gggcgtcctc ttcccgcc 360
 gttgctggcc aggtccttgc atcttccaat tactggagaa gccaatgaag aatgtgctgc 420
 catccatcac tgcggagctc ctcaagctgg gggcggctca ggctgacgct ggagaactga 480
 tcacgcagg agagctggc tccagacagg tgagcgagca attaactgag caagcagcaa 540
 ccttgggtt cctcctggat gctgtgacct tggatctgac cttcgggaag gaatttgcag 600
 aagcagtgga accaaaggag gtggctcagc aggaagaaga gagggccaga tctgtggtgg 660
 caagggctga gcagcagaag acggcggcca tcatctctgc cgaggcgac tccaaggcca 720
 cggagttcat cgccagctca gtggccaccg caggtgacgg cctgatcaag gcccacaagc 780
 tggAACCATG gaggacactg gccctccagc tctcagaact catccacctc atccacctgc 840
 ccgtggggac atctgtgctc ctccagctgc cccagcgcag gccgcccgtga cctgcaccc 900
 ctccagccaa ctgggccaca gcaccaatga cttttactac cgccttcctt ctgtccccac 960
 tccagaa 967

<210> 34

<211> 271

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
GM_11817402_A

<400> 34

Met Glu Thr Gln Leu Pro Ser Leu Pro Leu Ser Leu Ala Ser Ala Gly
1 5 10 15Gly Val Gly Asn Ser Ala Phe Tyr Asn Val Met Leu His Arg Glu Leu
20 25 30Ser Val Ile Phe Asp Gln Phe His Gly Ile Gln Asp Thr Val Ile Gly
35 40 45Glu Gly Thr His Phe Leu Ile Pro Trp Glu Lys Lys Pro Ile Ile Phe
50 55 60Asp Cys Cys Ser Arg Pro His Tyr Ala Pro Ile Ile Thr Val Ser Lys
65 70 75 80Asp Cys His His Val Thr Ile Thr Leu Gly Val Leu Phe Pro Pro Cys
85 90 95Cys Trp Pro Gly Pro Cys Ile Phe Gln Leu Leu Glu Lys Pro Met Lys
100 105 110Asn Val Leu Pro Ser Ile Thr Ala Glu Leu Leu Lys Leu Gly Ala Ala
115 120 125Gln Ala Asp Ala Gly Glu Leu Ile Thr Gln Gly Glu Leu Gly Ser Arg
130 135 140Gln Val Ser Glu Gln Leu Thr Glu Gln Ala Ala Thr Phe Gly Phe Leu
145 150 155 160Leu Asp Ala Val Thr Leu Asp Leu Thr Phe Gly Lys Glu Phe Ala Glu
165 170 175Ala Val Glu Pro Lys Glu Val Ala Gln Gln Glu Glu Arg Ala Arg
180 185 190Ser Val Val Ala Arg Ala Glu Gln Gln Lys Thr Ala Ala Ile Ile Ser
195 200 205Ala Glu Gly Asp Ser Lys Ala Thr Glu Phe Ile Ala Ser Ser Val Ala
210 215 220Thr Ala Gly Asp Gly Leu Ile Lys Ala His Lys Leu Glu Pro Trp Arg
225 230 235 240Thr Leu Ala Leu Gln Leu Ser Glu Leu Ile His Leu Ile His Leu Pro
245 250 255Val Gly Thr Ser Val Leu Leu Gln Leu Pro Gln Arg Arg Pro Pro
260 265 270

<210> 35
<211> 464
<212> PRT
<213> Rattus norvegicus

<400> 35
Met Val Leu Ala Phe Trp Leu Ala Phe Phe Thr Tyr Thr Trp Ile Thr
1 5 10 15
Leu Met Leu Asp Ala Ser Ala Val Lys Glu Pro His Gln Gln Cys Leu
20 25 30
Ser Ser Pro Lys Gln Thr Arg Ile Arg Glu Thr Arg Met Arg Lys Asp
35 40 45
Asp Leu Thr Lys Val Trp Pro Leu Lys Arg Glu Gln Leu Leu His Ile
50 55 60
Glu Asp His Asp Phe Ser Thr Arg Pro Gly Phe Gly Gly Ser Pro Val
65 70 75 80
Pro Val Gly Ile Asp Val Gln Val Glu Ser Ile Asp Ser Ile Ser Glu
85 90 95
Val Asn Met Asp Phe Thr Met Thr Phe Tyr Leu Arg His Tyr Trp Lys
100 105 110
Asp Glu Arg Leu Ser Phe Pro Ser Thr Thr Asn Lys Ser Met Thr Phe
115 120 125
Asp Arg Arg Leu Ile Gln Lys Ile Trp Val Pro Asp Ile Phe Phe Val
130 135 140
His Ser Lys Arg Ser Phe Ile His Asp Thr Thr Val Glu Asn Ile Met
145 150 155 160
Leu Arg Val His Pro Asp Gly Asn Val Leu Phe Ser Leu Arg Ile Thr
165 170 175
Val Ser Ala Met Cys Phe Met Asp Phe Ser Arg Phe Pro Leu Asp Thr
180 185 190
Gln Asn Cys Ser Leu Glu Leu Glu Ser Tyr Ala Tyr Asn Glu Glu Asp
195 200 205
Leu Met Leu Tyr Trp Lys His Gly Asn Lys Ser Leu Asn Thr Glu Glu
210 215 220
His Ile Ser Leu Ser Gln Phe Phe Ile Glu Glu Phe Ser Ala Ser Ser
225 230 235 240
Gly Leu Ala Phe Tyr Ser Ser Thr Gly Trp Tyr Tyr Arg Leu Phe Ile
245 250 255
Asn Phe Val Leu Arg Arg His Ile Phe Phe Phe Val Leu Gln Thr Tyr
260 265 270

Phe Pro Ala Met Leu Met Val Met Leu Ser Trp Val Ser Phe Trp Ile
 275 280 285
 Asp Arg Arg Ala Val Pro Ala Arg Val Ser Leu Gly Ile Thr Thr Val
 290 295 300
 Leu Thr Met Ser Thr Ile Val Thr Gly Val Ser Ala Ser Met Pro Gln
 305 310 315 320
 Val Ser Tyr Val Lys Ala Val Asp Val Tyr Met Trp Val Ser Ser Leu
 325 330 335
 Phe Val Phe Leu Ser Val Ile Glu Tyr Ala Ala Val Asn Tyr Leu Thr
 340 345 350
 Thr Val Glu Glu Trp Lys Gln Leu Asn Arg Arg Gly Lys Ile Ser Gly
 355 360 365
 Met Tyr Asn Ile Asp Ala Val Gln Ala Met Ala Phe Asp Gly Cys Tyr
 370 375 380
 His Asp Gly Glu Thr Asp Val Asp Gln Thr Ser Phe Phe Leu His Ser
 385 390 395 400
 Glu Glu Asp Ser Met Arg Thr Lys Phe Thr Gly Ser Pro Cys Ala Asp
 405 410 415
 Ser Ser Gln Ile Lys Arg Lys Ser Leu Gly Gly Asn Val Gly Arg Ile
 420 425 430
 Ile Leu Glu Asn Asn His Val Ile Asp Thr Tyr Ser Arg Ile Val Phe
 435 440 445
 Pro Val Val Tyr Ile Ile Phe Asn Leu Phe Tyr Trp Gly Ile Tyr Val
 450 455 460

<210> 36
 <211> 464
 <212> PRT
 <213> Rattus norvegicus

<400> 36
 Met Val Leu Ala Phe Trp Leu Ala Phe Phe Thr Tyr Thr Trp Ile Thr
 1 5 10 15
 Leu Met Leu Asp Ala Ser Ala Val Lys Glu Pro His Gln Gln Cys Leu
 20 25 30
 Ser Ser Pro Lys Gln Thr Arg Ile Arg Glu Thr Arg Met Arg Lys Asp
 35 40 45
 Asp Leu Thr Lys Val Trp Pro Leu Lys Arg Glu Gln Leu Leu His Ile
 50 55 60
 Glu Asp His Asp Phe Ser Thr Arg Pro Gly Phe Gly Gly Ser Pro Val
 65 70 75 80

Pro Val Gly Ile Asp Val Gln Val Glu Ser Ile Asp Ser Ile Ser Glu
 85 90 95

 Val Asn Met Asp Phe Thr Met Thr Phe Tyr Leu Arg His Tyr Trp Lys
 100 105 110

 Asp Glu Arg Leu Ser Phe Pro Ser Thr Thr Asn Lys Ser Met Thr Phe
 115 120 125

 Asp Arg Arg Leu Ile Gln Lys Ile Trp Val Pro Asp Ile Phe Phe Val
 130 135 140

 His Ser Lys Arg Ser Phe Ile His Asp Thr Thr Val Glu Asn Ile Met
 145 150 155 160

 Leu Arg Val His Pro Asp Gly Asn Val Leu Phe Ser Leu Arg Ile Thr
 165 170 175

 Val Ser Ala Met Cys Phe Met Asp Phe Ser Arg Phe Pro Leu Asp Thr
 180 185 190

 Gln Asn Cys Ser Leu Glu Leu Glu Ser Tyr Ala Tyr Asn Glu Glu Asp
 195 200 205

 Leu Met Leu Tyr Trp Lys His Gly Asn Lys Ser Leu Asn Thr Glu Glu
 210 215 220

 His Ile Ser Leu Ser Gln Phe Phe Ile Glu Glu Phe Ser Ala Ser Ser
 225 230 235 240

 Gly Leu Ala Phe Tyr Ser Ser Thr Gly Trp Tyr Tyr Arg Leu Phe Ile
 245 250 255

 Asn Phe Val Leu Arg Arg His Ile Phe Phe Phe Val Leu Gln Thr Tyr
 260 265 270

 Phe Pro Ala Met Leu Met Val Met Leu Ser Trp Val Ser Phe Trp Ile
 275 280 285

 Asp Arg Arg Ala Val Pro Ala Arg Val Ser Leu Gly Ile Thr Thr Val
 290 295 300

 Leu Thr Met Ser Thr Ile Val Thr Gly Val Ser Ala Ser Met Pro Gln
 305 310 315 320

 Val Ser Tyr Val Lys Ala Val Asp Val Tyr Met Trp Val Ser Ser Leu
 325 330 335

 Phe Val Phe Leu Ser Val Ile Glu Tyr Ala Ala Val Asn Tyr Leu Thr
 340 345 350

 Thr Val Glu Glu Trp Lys Gln Leu Asn Arg Arg Gly Lys Ile Ser Gly
 355 360 365

 Met Tyr Asn Ile Asp Ala Val Gln Ala Met Ala Phe Asp Gly Cys Tyr
 370 375 380

His Asp Gly Glu Thr Asp Val Asp Gln Thr Ser Phe Phe Leu His Ser
 385 390 395 400

Glu Glu Asp Ser Met Arg Thr Lys Phe Thr Gly Ser Pro Cys Ala Asp
 405 410 415

Ser Ser Gln Ile Lys Arg Lys Ser Leu Gly Gly Asn Val Gly Arg Ile
 420 425 430

Ile Leu Glu Asn Asn His Val Ile Asp Thr Tyr Ser Arg Ile Val Phe
 435 440 445

Pro Val Val Tyr Ile Ile Phe Asn Leu Phe Tyr Trp Gly Ile Tyr Val
 450 455 460

<210> 37

<211> 464

<212> PRT

<213> Rattus norvegicus

<400> 37

Met Val Leu Ala Phe Trp Leu Ala Phe Phe Thr Tyr Thr Trp Ile Thr
 1 5 10 15

Leu Met Leu Asp Ala Ser Ala Val Lys Glu Pro His Gln Gln Cys Leu
 20 25 30

Ser Ser Pro Lys Gln Thr Arg Ile Arg Glu Thr Arg Met Arg Lys Asp
 35 40 45

Asp Leu Thr Lys Val Trp Pro Leu Lys Arg Glu Gln Leu Leu His Ile
 50 55 60

Glu Asp His Asp Phe Ser Thr Arg Pro Gly Phe Gly Ser Pro Val
 65 70 75 80

Pro Val Gly Ile Asp Val Gln Val Glu Ser Ile Asp Ser Ile Ser Glu
 85 90 95

Val Asn Met Asp Phe Thr Met Thr Phe Tyr Leu Arg His Tyr Trp Lys
 100 105 110

Asp Glu Arg Leu Ser Phe Pro Ser Thr Thr Asn Lys Ser Met Thr Phe
 115 120 125

Asp Arg Arg Leu Ile Gln Lys Ile Trp Val Pro Asp Ile Phe Phe Val
 130 135 140

His Ser Lys Arg Ser Phe Ile His Asp Thr Thr Val Glu Asn Ile Met
 145 150 155 160

Leu Arg Val His Pro Asp Gly Asn Val Leu Phe Ser Leu Arg Ile Thr
 165 170 175

Val Ser Ala Met Cys Phe Met Asp Phe Ser Arg Phe Pro Leu Asp Thr
 180 185 190

Gln Asn Cys Ser Leu Glu Leu Glu Ser Tyr Ala Tyr Asn Glu Glu Asp
 195 200 205
 Leu Met Leu Tyr Trp Lys His Gly Asn Lys Ser Leu Asn Thr Glu Glu
 210 215 220
 His Ile Ser Leu Ser Gln Phe Phe Ile Glu Glu Phe Ser Ala Ser Ser
 225 230 235 240
 Gly Leu Ala Phe Tyr Ser Ser Thr Gly Trp Tyr Tyr Arg Leu Phe Ile
 245 250 255
 Asn Phe Val Leu Arg Arg His Ile Phe Phe Val Leu Gln Thr Tyr
 260 265 270
 Phe Pro Ala Met Leu Met Val Met Leu Ser Trp Val Ser Phe Trp Ile
 275 280 285
 Asp Arg Arg Ala Val Pro Ala Arg Val Ser Leu Gly Ile Thr Thr Val
 290 295 300
 Leu Thr Met Ser Thr Ile Val Thr Gly Val Ser Ala Ser Met Pro Gln
 305 310 315 320
 Val Ser Tyr Val Lys Ala Val Asp Val Tyr Met Trp Val Ser Ser Leu
 325 330 335
 Phe Val Phe Leu Ser Val Ile Glu Tyr Ala Ala Val Asn Tyr Leu Thr
 340 345 350
 Thr Val Glu Glu Trp Lys Gln Leu Asn Arg Arg Gly Lys Ile Ser Gly
 355 360 365
 Met Tyr Asn Ile Asp Ala Val Gln Ala Met Ala Phe Asp Gly Cys Tyr
 370 375 380
 His Asp Gly Glu Thr Asp Val Asp Gln Thr Ser Phe Phe Leu His Ser
 385 390 395 400
 Glu Glu Asp Ser Met Arg Thr Lys Phe Thr Gly Ser Pro Cys Ala Asp
 405 410 415
 Ser Ser Gln Ile Lys Arg Lys Ser Leu Gly Gly Asn Val Gly Arg Ile
 420 425 430
 Ile Leu Glu Asn Asn His Val Ile Asp Thr Tyr Ser Arg Ile Val Phe
 435 440 445
 Pro Val Val Tyr Ile Ile Phe Asn Leu Phe Tyr Trp Gly Ile Tyr Val
 450 455 460

<210> 38
 <211> 464
 <212> PRT
 <213> Rattus norvegicus

<400> 38
 Met Val Leu Ala Phe Trp Leu Ala Phe Phe Thr Tyr Thr Trp Ile Thr
 1 5 10 15

Leu Met Leu Asp Ala Ser Ala Val Lys Glu Pro His Gln Gln Cys Leu
 20 25 30

Ser Ser Pro Lys Gln Thr Arg Ile Arg Glu Thr Arg Met Arg Lys Asp
 35 40 45

Asp Leu Thr Lys Val Trp Pro Leu Lys Arg Glu Gln Leu Leu His Ile
 50 55 60

Glu Asp His Asp Phe Ser Thr Arg Pro Gly Phe Gly Gly Ser Pro Val
 65 70 75 80

Pro Val Gly Ile Asp Val Gln Val Glu Ser Ile Asp Ser Ile Ser Glu
 85 90 95

Val Asn Met Asp Phe Thr Met Thr Phe Tyr Leu Arg His Tyr Trp Lys
 100 105 110

Asp Glu Arg Leu Ser Phe Pro Ser Thr Thr Asn Lys Ser Met Thr Phe
 115 120 125

Asp Arg Arg Leu Ile Gln Lys Ile Trp Val Pro Asp Ile Phe Phe Val
 130 135 140

His Ser Lys Arg Ser Phe Ile His Asp Thr Thr Val Glu Asn Ile Met
 145 150 155 160

Leu Arg Val His Pro Asp Gly Asn Val Leu Phe Ser Leu Arg Ile Thr
 165 170 175

Val Ser Ala Met Cys Phe Met Asp Phe Ser Arg Phe Pro Leu Asp Thr
 180 185 190

Gln Asn Cys Ser Leu Glu Leu Glu Ser Tyr Ala Tyr Asn Glu Glu Asp
 195 200 205

Leu Met Leu Tyr Trp Lys His Gly Asn Lys Ser Leu Asn Thr Glu Glu
 210 215 220

His Ile Ser Leu Ser Gln Phe Phe Ile Glu Glu Phe Ser Ala Ser Ser
 225 230 235 240

Gly Leu Ala Phe Tyr Ser Ser Thr Gly Trp Tyr Tyr Arg Leu Phe Ile
 245 250 255

Asn Phe Val Leu Arg Arg His Ile Phe Phe Phe Val Leu Gln Thr Tyr
 260 265 270

Phe Pro Ala Met Leu Met Val Met Leu Ser Trp Val Ser Phe Trp Ile
 275 280 285

Asp Arg Arg Ala Val Pro Ala Arg Val Ser Leu Gly Ile Thr Thr Val
 290 295 300

Leu Thr Met Ser Thr Ile Val Thr Gly Val Ser Ala Ser Met Pro Gln
 305 310 315 320

Val Ser Tyr Val Lys Ala Val Asp Val Tyr Met Trp Val Ser Ser Leu
 325 330 335

Phe Val Phe Leu Ser Val Ile Glu Tyr Ala Ala Val Asn Tyr Leu Thr
 340 345 350

Thr Val Glu Glu Trp Lys Gln Leu Asn Arg Arg Gly Lys Ile Ser Gly
 355 360 365

Met Tyr Asn Ile Asp Ala Val Gln Ala Met Ala Phe Asp Gly Cys Tyr
 370 375 380

His Asp Gly Glu Thr Asp Val Asp Gln Thr Ser Phe Phe Leu His Ser
 385 390 395 400

Glu Glu Asp Ser Met Arg Thr Lys Phe Thr Gly Ser Pro Cys Ala Asp
 405 410 415

Ser Ser Gln Ile Lys Arg Lys Ser Leu Gly Gly Asn Val Gly Arg Ile
 420 425 430

Ile Leu Glu Asn Asn His Val Ile Asp Thr Tyr Ser Arg Ile Val Phe
 435 440 445

Pro Val Val Tyr Ile Ile Phe Asn Leu Phe Tyr Trp Gly Ile Tyr Val
 450 455 460

<210> 39
 <211> 392
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (111)
 <223> Any amino acid

<400> 39
 Met Asn Leu Asp Val Ala Lys Lys Pro Pro Arg Thr Ser Glu Arg Gln
 1 5 10 15

Ala Glu Ser Cys Gly Val Gly Gln Gly His Ala Glu Asn Gln Cys Val
 20 25 30

Ser Cys Arg Ala Gly Thr Tyr Tyr Asp Gly Ala Arg Glu Arg Cys Ile
 35 40 45

Leu Cys Pro Asn Gly Thr Phe Gln Asn Glu Glu Gly Gln Met Thr Cys
 50 55 60

Glu Pro Cys Pro Arg Pro Gly Asn Ser Gly Ala Leu Lys Thr Pro Glu
 65 70 75 80

Ala Trp Asn Met Ser Glu Cys Gly Gly Leu Cys Gln Pro Thr Glu Tyr
 85 90 95

 Ser Ala Asp Gly Phe Ala Pro Cys Gln Leu Cys Ala Leu Gly Xaa Phe
 100 105 110

 Gln Pro Glu Ala Gly Arg Thr Ser Cys Phe Pro Cys Gly Gly Leu
 115 120 125

 Ala Thr Lys His Gln Gly Ala Thr Ser Phe Gln Asp Cys Glu Thr Arg
 130 135 140

 Val Gln Cys Ser Pro Gly His Phe Tyr Asn Thr Thr Thr His Arg Cys
 145 150 155 160

 Ile Arg Cys Pro Val Gly Thr Tyr Gln Pro Glu Phe Gly Lys Asn Asn
 165 170 175

 Cys Val Ser Cys Pro Gly Asn Thr Thr Asp Phe Asp Gly Ser Thr
 180 185 190

 Asn Ile Thr Gln Cys Lys Asn Arg Arg Cys Gly Gly Glu Leu Gly Asp
 195 200 205

 Phe Thr Gly Tyr Ile Glu Ser Pro Asn Tyr Pro Gly Asn Tyr Pro Ala
 210 215 220

 Asn Thr Glu Cys Thr Trp Thr Ile Asn Pro Pro Pro Lys Arg Arg Ile
 225 230 235 240

 Leu Ile Val Val Pro Glu Ile Phe Leu Pro Ile Glu Asp Asp Cys Gly
 245 250 255

 Asp Tyr Leu Val Met Arg Lys Thr Ser Ser Ser Asn Ser Val Thr Thr
 260 265 270

 Tyr Glu Thr Cys Gln Thr Tyr Glu Arg Pro Ile Ala Phe Thr Ser Arg
 275 280 285

 Ser Lys Lys Leu Trp Ile Gln Phe Lys Ser Asn Glu Gly Asn Ser Ala
 290 295 300

 Arg Gly Phe Gln Val Pro Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu
 305 310 315 320

 Leu Ile Glu Asp Ile Val Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn
 325 330 335

 His Gln Glu Ile Leu Lys Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp
 340 345 350

 Val Leu Ala His Pro Gln Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser
 355 360 365

 Arg Glu Met Phe Pro Arg Ser Phe Ile Arg Leu Leu Arg Ser Lys Val
 370 375 380

Ser Arg Phe Leu Arg Pro Tyr Lys
385 390

<210> 40
<211> 283
<212> PRT
<213> Rattus norvegicus

<400> 40
Glu Val Asn Gly Ile Leu Met Ser Lys Leu Met Ser Asp Asn Trp Asp
1 5 10 15

Lys Ile Trp Asn Phe Gln Ala Lys Pro Asp Asp Leu Leu Ile Ala Thr
20 25 30

Tyr Ala Lys Ala Gly Thr Thr Trp Thr Gln Glu Ile Val Asp Met Ile
35 40 45

Gln Asn Asp Gly Asp Val Gln Lys Cys Gln Arg Ala Asn Thr Tyr Asp
50 55 60

Arg His Pro Phe Ile Glu Trp Thr Leu Pro Ser Pro Leu Asn Ser Gly
65 70 75 80

Leu Asp Leu Ala Asn Lys Met Pro Ser Pro Arg Thr Leu Lys Thr His
85 90 95

Leu Pro Val His Met Leu Pro Pro Ser Phe Trp Lys Glu Asn Ser Lys
100 105 110

Ile Ile Tyr Val Ala Arg Asn Ala Lys Asp Cys Leu Val Ser Tyr Tyr
115 120 125

Tyr Phe Ser Arg Met Asn Lys Met Leu Pro Asp Pro Gly Thr Leu Gly
130 135 140

Glu Tyr Ile Glu Gln Phe Lys Ala Gly Lys Val Leu Trp Gly Ser Trp
145 150 155 160

Tyr Asp His Val Lys Gly Trp Trp Asp Val Lys Asp Gln His Arg Ile
165 170 175

Leu Tyr Leu Phe Tyr Glu Asp Met Lys Glu Asp Pro Lys Arg Glu Ile
180 185 190

Lys Lys Ile Ala Lys Phe Leu Glu Lys Asp Ile Ser Glu Glu Val Leu
195 200 205

Asn Lys Ile Ile Tyr His Thr Ser Phe Asp Val Met Lys Glu Asn Pro
210 215 220

Met Ala Asn Tyr Thr Thr Leu Pro Ser Ser Ile Met Asp His Ser Ile
225 230 235 240

Ser Pro Phe Met Arg Lys Gly Met Pro Gly Asp Trp Lys Asn Tyr Phe
245 250 255

Thr Val Ala Gln Ser Glu Asp Phe Asp Glu Asp Tyr Arg Arg Lys Met
 260 265 270

Ala Gly Ser Asn Ile Thr Phe Arg Thr Glu Ile
 275 280

<210> 41
 <211> 285
 <212> PRT
 <213> Homo sapiens

<400> 41
 Met Lys Asp Arg Leu Ala Glu Leu Leu Asp Leu Ser Lys Gln Tyr Asp
 1 5 10 15

Gln Gln Phe Pro Asp Gly Asp Asp Glu Phe Asp Ser Pro His Glu Asp
 20 25 30

Ile Val Phe Glu Thr Asp His Ile Leu Glu Ser Leu Tyr Arg Asp Ile
 35 40 45

Arg Asp Ile Gln Asp Glu Asn Gln Leu Leu Val Ala Asp Val Lys Arg
 50 55 60

Leu Gly Lys Gln Asn Ala Arg Phe Leu Thr Ser Met Arg Arg Leu Ser
 65 70 75 80

Ser Ile Lys Arg Asp Thr Asn Ser Ile Ala Lys Ala Ile Lys Ala Arg
 85 90 95

Gly Glu Val Ile His Cys Lys Leu Arg Ala Met Lys Glu Leu Ser Glu
 100 105 110

Ala Ala Glu Ala Gln His Gly Pro His Ser Ala Val Ala Arg Ile Ser
 115 120 125

Arg Ala Gln Tyr Asn Ala Leu Thr Leu Thr Phe Gln Arg Ala Met His
 130 135 140

Asp Tyr Asn Gln Ala Glu Met Lys Gln Arg Asp Asn Cys Lys Ile Arg
 145 150 155 160

Ile Gln Arg Gln Leu Glu Ile Met Gly Lys Glu Val Ser Gly Asp Gln
 165 170 175

Ile Glu Asp Met Phe Glu Gln Gly Lys Trp Asp Val Phe Ser Glu Asn
 180 185 190

Leu Leu Ala Asp Val Lys Gly Ala Arg Ala Ala Leu Asn Glu Ile Glu
 195 200 205

Ser Arg His Arg Glu Leu Leu Arg Leu Glu Ser Arg Ile Arg Asp Val
 210 215 220

His Glu Leu Phe Leu Gln Met Ala Val Leu Val Glu Lys Gln Ala Asp
 225 230 235 240

Thr Leu Asn Val Ile Glu Leu Asn Val Gln Lys Thr Val Asp Tyr Thr
 245 250 255

Gly Gln Ala Lys Ala Gln Val Arg Lys Ala Val Gln Tyr Glu Glu Lys
 260 265 270

Asn Pro Cys Arg Thr Leu Cys Cys Phe Cys Cys Pro Cys
 275 280 285

<210> 42
 <211> 285
 <212> PRT
 <213> Homo sapiens

<400> 42
 Met Lys Asp Arg Leu Ala Glu Leu Leu Asp Leu Ser Lys Gln Tyr Asp
 1 5 10 15

Gln Gln Phe Pro Asp Gly Asp Asp Glu Phe Asp Ser Pro His Glu Asp
 20 25 30

Ile Val Phe Glu Thr Asp His Ile Leu Glu Ser Leu Tyr Arg Asp Ile
 35 40 45

Arg Asp Ile Gln Asp Glu Asn Gln Leu Leu Val Ala Asp Val Lys Arg
 50 55 60

Leu Gly Lys Gln Asn Ala Arg Phe Leu Thr Ser Met Arg Arg Leu Ser
 65 70 75 80

Ser Ile Lys Arg Asp Thr Asn Ser Ile Ala Lys Ala Ile Lys Ala Arg
 85 90 95

Gly Glu Val Ile His Cys Lys Leu Arg Ala Met Lys Glu Leu Ser Glu
 100 105 110

Ala Ala Glu Ala Gln His Gly Pro His Ser Ala Val Ala Arg Ile Ser
 115 120 125

Arg Ala Gln Tyr Asn Ala Leu Thr Leu Thr Phe Gln Arg Ala Met His
 130 135 140

Asp Tyr Asn Gln Ala Glu Met Lys Gln Arg Asp Asn Cys Lys Ile Arg
 145 150 155 160

Ile Gln Arg Gln Leu Glu Ile Met Gly Lys Glu Val Ser Gly Asp Gln
 165 170 175

Ile Glu Asp Met Phe Glu Gln Gly Lys Trp Asp Val Phe Ser Glu Asn
 180 185 190

Leu Leu Ala Asp Val Lys Gly Ala Arg Ala Ala Leu Asn Glu Ile Glu
 195 200 205

Ser Arg His Arg Glu Leu Leu Arg Leu Glu Ser Arg Ile Arg Asp Val
 210 215 220

His Glu Leu Phe Leu Gln Met Ala Val Leu Val Glu Lys Gln Ala Asp
225 230 235 240

Thr Leu Asn Val Ile Glu Leu Asn Val Gln Lys Thr Val Asp Tyr Thr
245 250 255

Gly Gln Ala Lys Ala Gln Val Arg Lys Ala Val Gln Tyr Glu Glu Lys
260 265 270

Asn Pro Cys Arg Thr Leu Cys Cys Phe Cys Cys Pro Cys
275 280 285

<210> 43

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 43

ttggaagaga tggtcctggc ttcc

24

<210> 44

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 44

ttcataggat tctcagctgt gtgagtg

27

<210> 45

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 45

ttggaagaga tggtcctggc ttcc

24

<210> 46

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 46
ttcataggat tctcagctgt gtgagtg 27

<210> 47
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 47
gtgtgttcct ctcgactgtg ga 22

<210> 48
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 48
gacccttggaa ccctacttca aa 22

<210> 49
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe

<400> 49
ccccgatcca gaatggcttc atga 24

<210> 50
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe

<400> 50
tgtgccgagg gcaacg 16

<210> 51
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe

<400> 51
tagctgcccc tcatgttgac acagctct 28

<210> 52
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe

<400> 52
agaaggccttc ccggcagt 18

<210> 53
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe

<400> 53
cttgtgggcc agctcataat c 21

<210> 54
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe

<400> 54
accgcttcct gctgcgcctg 20

<210> 55
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe

<400> 55
gatgctcaga aagtccatca acc 23

<210> 56
<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe

<400> 56
cttatgagac ctgccagacc ta

22

<210> 57
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe

<400> 57
cttcactgcc cgttccagga agct

24

<210> 58
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe

<400> 58
ctcgcttgtc ttgaagttga tc

22